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Db      466 TTTCTCCGGAGATCATCTCTGAGCTGACTTCTGCGCAGACGACCTTCATATATGCGACAG 525
Qy      421 GATGTGAAACCTGAAAACCTCTCTGCTGAGAGAGAAACAATCTCGCATATCGAGACTTT 480
Db      526 GATGTGAAACCTGAAAACCTCTCTGCTGAGAGAGAAACAATCTCGCATATCGAGACTTT 585
Qy      481 GGCATGAGCGTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db      586 GGCATGAGCGTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645
Qy      541 TAGCGCTGCCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db      646 TACCGCTGCCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 705
Qy      601 AGCTGCGGCGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db      706 AGCTGCGGCGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 765
Qy      661 TTGCGACAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db      766 TTGCGACAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 825
Qy      721 CCGGACCTGGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db      826 CCGGACCTGGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885
Qy      781 CTAGAGCACAATTGAGAAACAATATATATATATATATATATATATATATATATATATAT 840
Db      886 CTAGAGCACAATTGAGAAACAATATATATATATATATATATATATATATATATATATAT 945
Qy      841 CAGGCCATTTCTCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db      946 CAGGCCATTTCTCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1005
Qy      901 GAGCTGCTGAGCAGCAGATGCACTCACTGAGCTGCTTCCGAGACCGCAACAAGCTGTGAG 960
Db      1006 GAGCTGCTGAGCAGCAGATGCACTCACTGAGCTGCTTCCGAGACCGCAACAAGCTGTGAG 1065
Qy      961 GACTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db      1066 GACTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1125
Qy      1021 AAAAGAAAGTACCCGAGCCGAGAGAGATGAGAGACCTGCCCCCGGAGAACGATAGACCTT 1080
Db      1126 AAAAGAAAGTACCCGAGCCGAGAGAGATGAGAGACCTGCCCCCGGAGAACGATAGACCTT 1185
Qy      1081 CCCCAGAAAGCTGTGACTCTCCGATGCTGAACCGGCAAGCGCGCGCCAGAACCG 1140
Db      1186 CCCCAGAAAGCTGTGACTCTCCGATGCTGAACCGGCAAGCGCGCGCCAGAACCG 1245
Qy      1141 AAATCCATGAGAGTGTCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db      1246 AAGTCCATGAGAGTGTCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1305
Qy      1201 ATTGAGATGAGCCGAGCAGCGCAGAGAGTCTCGGTCAATCAGCGGTGCTCTCAGAGCTTT 1260
Db      1306 ATTGAGATGAGCCGAGCAGCGCAGAGAGTCTCGGTCAATCAGCGGTGCTCTCAGAGCTTT 1365
Qy      1261 TCCACAGAGCCCACTCAGACAGCCCGCGGTGACCCCTCAACCCCTCAACAGAGGCAATGCC 1320
Db      1366 TCCACAGAGCCCACTCAGACAGCCCGCGGTGACCCCTCAACCCCTCAACAGAGGCAATGCC 1425
Qy      1321 CTCGCCACCCCAAGAGGAGACACTGTGCACAGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db      1426 CTCGCCACCCCAAGAGGAGACACTGTGCACAGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1485
Qy      1381 AACCCCAAGCCCGCTCCAGCGCCCAAGCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db      1486 AACCCCAAGCCCGCTCCAGCGCCCAAGCGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1545
Qy      1441 TCCATCAGAGAACAGCTTTGAGGCTCAACCCGCTTCAACCGCGGAGAACTGCAGAGTTCCG 1500

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Db      1546 TCCATCAGAGAACAGCTTTGAGGCTCAACCCGCTTCCACCGCGGAGAACTGCAAGTTCCG 1605
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Db      1606 AGCCGAGAGAGAGATGTCACCACTGACACAGAGTGTGTCCAGAGCTGAGAGAGAGTCC 1665
Qy      1561 TGGTTTGGGAACCTTCAATCAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db      1666 TGGTTTGGGAACCTTCAATCAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1725
Qy      1621 AAACCTGAGCTGCATCAAGGCTGACATGATGACAGCCCTTCTGATTCAGATTCAGCTTC 1680
Db      1726 AAACCTGAGCTGCATCAAGGCTGACATGATGACAGCCCTTCTGATTCAGATTCAGCTTC 1785
Qy      1681 AGCCACAGCTGCATCTCCCAACAGAGCTTCCGAGCGAGTCAAGGCTCAAGGCGAGGAGGCA 1740
Db      1786 AGCCACAGCTGCATCTCCCAACAGAGCTTCCGAGCGAGTCAAGGCTCAAGGCGAGGAGGCA 1845
Qy      1741 GCGGTGTTCCAGAAAGCGGTCAAGTTCAGAGTGAATATCACTCACTCACTCACTCACTCACT 1800
Db      1846 GCGGTGTTCCAGAAAGCGGTCAAGTTCAGAGTGAATATCACTCACTCACTCACTCACTCACT 1905
Qy      1801 GCGCAGAGAGAGAGAGAGAGATCTACTCTGCTCACTTCACTTCACTTCTGAGAGCCCAAGCGGT 1860
Db      1906 GCGCAGAGAGAGAGAGAGAGATCTACTCTGCTCACTTCACTTCACTTCTGAGAGCCCAAGCGGT 1965
Qy      1861 CGCTTCAAGAGAGGTGTGTGAGAGACATCCAGGCCAGGTGCTGAGAGACACAGAGCCGCT 1920
Db      1966 CGCTTCAAGAGAGGTGTGTGAGAGACATCCAGGCCAGGTGCTGAGAGACACAGAGCCGCT 2025
Qy      1921 GCGGCCAGCAGCTTGTGAGACACCACTACTGATGAGAAATGATGAGAGAGAGAGAGAGAGAG 1980
Db      2026 GCGGCCAGCAGCTTGTGAGACACCACTACTGATGAGAAATGATGAGAGAGAGAGAGAGAGAG 2085
Qy      1981 AAATGTGAATTAATCCGAAAAGTTAA 2007
Db      2086 AAATGTGAATTAATCCGAAAAGTTAA 2112

RESULT 2
US-09-930-181-3
; Sequence 3, Application US/09930181
; Patent No. 6455292
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 VI
; CURRENT APPLICATION NUMBER: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3364
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (482)..(2239)
US-09-930-181-3

Query/ Match      99.3%; Score 1993; DB 4; Length 3364;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2007; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy      1 ATGACATGAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db      229 ATGACATGAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 288
Qy      61 CTGAGAGAGAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db      289 CTGAGAGAGAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 348
Qy      121 ACCTGCCAGAGAGTGGCCATCAAGATGATCAACCGGTGAGAGAGAGAGAGAGAGAGAGAG 180

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Db 349 ACCGCGAGAGGAGGCGATCAAGATGTCACCGTAGAAGCTCAGCGGTGGAGCTG 408  
Qy 181 ATGAAGGTGAGGAGGAGATCGCGATCCTGAAGCTCATTTAGACACCCCACTCTAAAG 240  
Db 409 ATGAAGGTGAGGAGGAGATCGCGATCCTGAAGCTCATTTAGACACCCCACTCTAAAG 468  
Qy 241 CTGACGACGCTTTATGAAAAAATAATTTT---GTACTGTGTGTAGAACACGCTGTC 296  
Db 469 CTGACGACGCTTTATGAAAAAATAATTTTGTAGTAACTGTGTGTAGAACACGCTGTC 528  
Qy 297 AGGTGTGAGGCTCTTCACTACCTGTGTGAGAGAGAGGAGGCTGACGCTTAAGAGAGCTG 356  
Db 529 AGGTGTGAGGCTCTTCACTACCTGTGTGAGAGAGAGGAGGCTGACGCTTAAGAGAGCTG 588  
Qy 357 GAAGTCTTCCGAGAGATCACTCTGTGCGCTGGAATTGTGCAAGCCACTTCATATGCCA 416  
Db 589 GAAGTCTTCCGAGAGATCACTCTGTGCGCTGGAATTGTGCAAGCCACTTCATATGCCA 648  
Qy 417 CAGGATCTGAAACTGAAAACTCTGTGTGAGACGAGAGAAACAATCCGCAATCCGAGA 476  
Db 649 CAGGATCTGAAACTGAAAACTCTGTGTGAGACGAGAGAAACAATCCGCAATCCGAGA 708  
Qy 477 CTTGGATGAGCGCTCCCTGAGGTTGAGCAAGGCTGTTGAGACGAGCTGTGGTCCCG 536  
Db 709 CTTGGATGAGCGCTCCCTGAGGTTGAGCAAGGCTGTTGAGACGAGCTGTGGTCCCG 768  
Qy 537 CCACTAGCGCTGCCCGAGGTGATCCGGGAGAGAAATATGACGCGCGGAGAGCGGAGCT 596  
Db 769 CCACTAGCGCTGCCCGAGGTGATCCGGGAGAGAAATATGACGCGCGGAGAGCGGAGCT 828  
Qy 597 GTGAGGTGAGGAGGCTACCTGTTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 656  
Db 829 GTGAGGTGAGGAGGCTACCTGTTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 888  
Qy 657 CAATTTGCGACAGCTGTGTGAGAGAGTGAAGCGGAGGCTGTTCACATGCGGACATTTAT 716  
Db 889 CAATTTGCGACAGCTGTGTGAGAGAGTGAAGCGGAGGCTGTTCACATGCGGACATTTAT 948  
Qy 717 CCGGCGCGAGCTGCGAGAGTCTGCTACCGGAGGAGATGAGAGTGTGACCGCGGAGCGCT 776  
Db 949 CCGGCGCGAGCTGCGAGAGTCTGCTACCGGAGGAGATGAGAGTGTGACCGCGGAGCGCT 1008  
Qy 777 CACGCTAGAGCACTTGTGAGAAACATATGATGATGAGGAGGAGAGATGAGCGGAGCG 836  
Db 1009 CACGCTAGAGCACTTGTGAGAAACATATGATGATGAGGAGGAGAGATGAGCGGAGCG 1068  
Qy 837 AGAGCAGCCACTTCTGTGCAAGGTGTGAGATCCGCTCCGCTCCAGCTGTGAGAGCATCGA 896  
Db 1069 AGAGCAGCCACTTCTGTGCAAGGTGTGAGATCCGCTCCGCTCCAGCTGTGAGAGCATCGA 1128  
Qy 897 CCGGAGGAGTGTGAGACGAGTCACTGAGGCTGTGCTGCGAGACGCGAACAAGCTGCT 956  
Db 1129 CCGGAGGAGTGTGAGACGAGTCACTGAGGCTGTGCTGCGAGACGCGAACAAGCTGCT 1188  
Qy 957 GCAGAGCTGTGTGTGAGAGAGAAACAAGAGAGATGATTTACTTCTCTCTCTGGA 1016  
Db 1189 GCAGAGCTGTGTGTGAGAGAGAAACAAGAGAGATGATTTACTTCTCTCTCTGGA 1248  
Qy 1017 CCGGAGAGAAAGTATCCCGAGGCGAGAGAGATGAGAGATCCCGCGCGGAGAAACAAGATGA 1076  
Db 1249 CCGGAGAGAAAGTATCCCGAGGCGAGAGAGATGAGAGATCCCGCGCGGAGAAACAAGATGA 1308  
Qy 1077 CCGTCTCCCGAGAGGCTGTGAGTCTCCGAGTGTGTAACCGGACGCGGAGGCGGCGAGA 1136  
Db 1309 CCGTCTCCCGAGAGGCTGTGAGTCTCCGAGTGTGTAACCGGACGCGGAGGCGGCGAGA 1368  
Qy 1137 ACAGAAATTCATGAGAGTGTCTACGCTGTGAGAGAGGAGGCTCCCGGCTGTGAGGCGG 1196  
Db 1369 ACAGAAATTCATGAGAGTGTCTACGCTGTGAGAGAGGAGGCTCCCGGCTGTGAGGCGG 1428  
Qy 1197 GGCCATTGAGATGCGGAGCAAGGAGTGTGCTGATCAGCGGAGCTCTCTCAGG 1256

Db 1429 GGCCATTGAGATGCGGAGCAAGGCGGAGAGAGTGTGCTGATCAGCGGTGCTCTCAGG 1488  
Qy 1257 CTTTTCACACAGCCCACTCAGAGAGCCCGGAGTGAACCTTCAACCCCTTCAACCAAGGAG 1316  
Db 1489 CTTTTCACACAGCCCACTCAGAGAGCCCGGAGTGAACCTTCAACCCCTTCAACCAAGGAG 1548  
Qy 1317 TCCCTTCCCGACCCCGAGGAGGAGCACTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGG 1376  
Db 1549 TCCCTTCCCGACCCCGAGGAGGAGCACTGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGG 1608  
Qy 1377 GCCAACCAGAGCCCGGCTCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1436  
Db 1609 GCCAACCAGAGCCCGGCTCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1668  
Qy 1437 CAATTCATGAGAGAGAGCTTTCTGAGCTCAACCCGCTTCAACCGCGGAGAACTCAAGT 1496  
Db 1669 CAATTCATGAGAGAGAGCTTTCTGAGCTCAACCCGCTTCAACCGCGGAGAACTCAAGT 1728  
Qy 1497 TCCGAGGCGGAGAGAGATGTCACACTGACACAGAGTGTGCCAGAGCTGCGGAGAGAA 1556  
Db 1729 TCCGAGGCGGAGAGAGATGTCACACTGACACAGAGTGTGCCAGAGCTGCGGAGAGAA 1788  
Qy 1557 GTCTGTGTTGGAACTTCATCAGCTGTGAGAGAGAGAGAGAGAGATCTTGTGTATCAA 1616  
Db 1789 GTCTGTGTTGGAACTTCATCAGCTGTGAGAGAGAGAGAGAGAGATCTTGTGTATCAA 1848  
Qy 1617 AGACAAACCTCTGAGACTTCATGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1676  
Db 1849 AGACAAACCTCTGAGACTTCATGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1908  
Qy 1677 TCTCAGGCAAGAGCTCATCTCCCAAGAGTTCGGGCGGAGTCAAGAGCCACGAGGAG 1736  
Db 1909 TCTCAGGCAAGAGCTCATCTCCCAAGAGTTCGGGCGGAGTCAAGAGCCACGAGGAG 1968  
Qy 1737 GCCAGCGCTTTCAGAGAGCGGTAAGTTTCAAGTTGATATCACTTACAGGAGGAGTGG 1796  
Db 1969 GCCAGCGCTTTCAGAGAGCGGTAAGTTTCAAGTTGATATCACTTACAGGAGGAGTGG 2028  
Qy 1797 GAGGAGGAG 1856  
Db 2029 GAGGAGGAG 2088  
Qy 1857 CCGTGTTCAGAGAGGAGTGTGAGAGACATCCAGGCGGAGGCTGTGAGAGACACGAGCC 1916  
Db 2089 CCGTGTTCAGAGAGGAGTGTGAGAGACATCCAGGCGGAGGCTGTGAGAGACACGAGCC 2148  
Qy 1917 GCGTGGGCGGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1976  
Db 2149 GCGTGGGCGGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2208  
Qy 1977 TTCGAATGTGAGATTTATCCGAGAAAGTTAA 2007  
Db 2209 TTCGAATGTGAGATTTATCCGAGAAAGTTAA 2239

RESULT 3  
US-08-557-006C-38  
; Sequence 38, Application US/08557006C  
; Patent No. 6258547  
; GENERAL INFORMATION:  
; APPLICANT: Beri, Rajindar K.  
; APPLICANT: Carling, David  
; APPLICANT: Forster, Robert A.  
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE  
; FILE REFERENCE: NGAP/PHM37588/UST  
; CURRENT APPLICATION NUMBER: US/08/557,006C  
; CURRENT FILING DATE: 1996-03-06  
; PRIOR APPLICATION NUMBER: PCT/GB94/01093  
; PRIOR FILING DATE: 1994-05-20  
; PRIOR APPLICATION NUMBER: GB 9310489.1  
; PRIOR FILING DATE: 1993-05-21  
; PRIOR APPLICATION NUMBER: GB 9318010.7  
; PRIOR FILING DATE: 1993-08-31

NUMBER OF SEQ ID NOS: 44  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO: 38  
 LENGTH: 1742  
 TYPE: DNA  
 ORGANISM: Human AMP protein kinase  
 US-08-557-006C-38

Query Match 11.2%; Score 225.4; DB 3; Length 1742;  
 Best Local Similarity 56.5%; Pred. No. 3.8e-42;  
 Matches 440; Conservative 0; Mismatches 336; Indels 3; Gaps 1;

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Qy 42 GTATGTTGGGCCCCCCTAAGCGCTGAGAGAGAGCTGGGGAAGGGGAGAGAGAGTGTGTA 101
Db 33 GAAGATGGAACACTACGTGCTGGGAGACCCCTGGGCTGGGACCTTGGGCAAAATGAA 92
Qy 102 GCTGGGGTTCACTGCTGCACTTCCAGAGGTGGCCATCAGATCGTCAACCGTGAGAA 161
Db 93 GATTGGAAGACATCAATTGACAGGCCATAAGTGGCAGTTAAGATCTTAATATGACAGAA 152
Qy 162 GCTCAGGAGTGGTGTGATG--AAGTGGAGCGGAGATGCGCATCTGAGAGCTCAT 218
Db 153 GATTCGAGTTTAAATGTGTGGAATAAATGAAATCAAAATCTTAACCTCTT 212
Qy 219 TGAGCACCCTCCCTCTAAAGCTGACAGAGCTTTATGAAAAAATAATTTGTAAGT 278
Db 213 TCGCATCTCATATTATTCACCAAGTATGACAGCATCCCAAGACTTTTAT 272
Qy 279 GTGTCTGAACACGTGTGAGTGTGAGTCTTGTGACTTCTGTTGAAAGAGGGAGCT 338
Db 273 GTTATGGAATATGTGTGGAAGGTGAATGTGTGACTCATCTGTAAACACGGAGGGT 332
Qy 339 GAGCCCTAAGAGGCTCGAAGTCTTCCGGCAGATCATCTGCGCTGAGCTTCTGCA 398
Db 333 TGAAGAGTGAAGCTGCGCGCTCTTCCAGCAGATTCGTCTGCGTGAACATCTGCA 392
Qy 399 CAGCCATCCATATGACAGAGGATCTGAAACCTGTAACCTCTGCTGAGAGAGAA 458
Db 393 CAGGACATGTGTGTCACAGGGACCTGAAGCCAGAAAGTGTGCTGAGACCCAGAT 452
Qy 459 CAACATCCGATGCGACACTTGGCATGCGGTGCTGCGAGTGTGGAGACAGCTGTGGA 518
Db 453 GAATGCTAAGTACTGCTTTCGACTCTCTTAATATGATGTCAGATGTGAATTTCTACG 512
Qy 519 GACCACTGTGTGCTCCCACTACGCTGCTCCGAGGTATCCGGGGGAGAGATGTA 578
Db 513 AACTAGCTGTGATCGCAAAATATGACAGCCGAGGTATCTCAGGAAGCTGTATGC 572
Qy 579 CGGCGGAGAGCGAGCTGTGAGACTGCGGCTCATTCCTGTGCGCTGTGGTGGGCG 638
Db 573 GGGTCTGAGGTGATATCTGAGAGCTGTGTATCTGTATGCCCTTCTGTGACAC 632
Qy 639 TCTGCCCTTGCAGATGACAACTTGCAGACAGTGTGAGAGAGGTGAAGCGGGCGTGT 698
Db 633 CTTCCCTGTGACATGAGAGAGAGCTGTGAGCTTAAAGAGATCCGAGGGGTGT 692
Qy 699 CCACATGCGCATTTTATCCCGCCGACGTGCAAGTCTGTACGGGGGAGATGAGAGT 758
Db 693 CTACATCCCGAGATATCAACCTGTATTTGCCACCTGTGTGACAGATGTGAGAGT 752
Qy 759 GAGAGCGGACGAGCGGCTGACGCTAGAGCATTCAGAAACATATGATATAGAGG 817
Db 753 GAGACCTTGAAGGAGAGCACTATCAAGACATACAGAGCATGAATGTTAAACAG 811

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## RESULT 4

US-08-557-006C-39  
 Sequence 39, Application US/08557006C

Patent No. 6258547  
 GENERAL INFORMATION:  
 APPLICANT: Bertl, Rajindar K.  
 APPLICANT: Carling, David  
 APPLICANT: Forde, Robert A.

TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE  
 FILE REFERENCE: NGA/P/PH37589/UST  
 CURRENT APPLICATION NUMBER: US/08/557,006C  
 CURRENT FILING DATE: 1996-03-06  
 PRIOR APPLICATION NUMBER: PCT/GB94/01093  
 PRIOR FILING DATE: 1994-05-20  
 PRIOR APPLICATION NUMBER: GB 9310489.1  
 PRIOR FILING DATE: 1993-05-21  
 PRIOR APPLICATION NUMBER: GB 9318010.7  
 PRIOR FILING DATE: 1993-08-31  
 NUMBER OF SEQ ID NOS: 44  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO: 39  
 LENGTH: 2652  
 TYPE: DNA  
 ORGANISM: Rat  
 FEATURE:  
 NAME/KEY: gene  
 LOCATION: (1)..  
 OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -  
 OTHER INFORMATION: fragment begins at nucleotide 24 and ends with  
 OTHER INFORMATION: nucleotide 1765  
 US-08-557-006C-39

Query Match 11.2%; Score 225.4; DB 3; Length 2652;  
 Best Local Similarity 56.5%; Pred. No. 4.4e-42;  
 Matches 440; Conservative 0; Mismatches 336; Indels 3; Gaps 1;

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Qy 42 GTATGTTGGGCCCCCCTAAGCGCTGAGAGAGAGCTGGGGAAGGGGAGAGAGTGTGTA 101
Db 40 GAAGATGGAACACTACGTGCTGGGAGACCCCTGGGCTGGGACCTTGGGCAAAATGAA 99
Qy 102 GCTGGGGTTCACTGCTGCACTTCCAGAGGTGGCCATCAGATCGTCAACCGTGAGAA 161
Db 100 GATTGGAAGACATCAATTGACAGGCCATAAGTGGCAGTTAAGATCTTAATATGACAGAA 159
Qy 162 GCTCAGGAGTGGTGTGATG--AAGTGGAGCGGAGATGCGCATCTGAGAGCTCAT 218
Db 160 GATTCGAGTTTAAATGTGTGGAATAAATGAAATCAAAATCTTAACCTCTT 219
Qy 219 TGAGCACCCTCCCTCTAAAGCTGACAGAGCTTTATGAAAAAATAATTTGTAAGT 278
Db 220 TCGCATCTCATATTATTCACCAAGTATGACAGCATCCCAAGACTTTTAT 279
Qy 279 GTGTCTGAACACGTGTGAGTGTGAGTCTTGTGACTTCTGTTGAAAGAGGGAGCT 338
Db 280 GTTATGGAATATGTGTGGAAGGTGAATGTGTGACTCATCTGTAAACACGGAGGGT 339
Qy 339 GAGCCCTAAGAGGCTCGAAGTCTTCCGGCAGATCATCTGCGCTGAGCTTCTGCA 398
Db 340 TGAAGAGTGAAGCTGCGCGCTCTTCCAGCAGATTCGTCTGCGTGAACATCTGCA 399
Qy 399 CAGCCATCCATATGACAGAGGATCTGAAACCTGTAACCTCTGCTGAGAGAGAA 458
Db 400 CAGGACATGTGTGTCACAGGGACCTGAAGCCAGAAAGTGTGCTGAGACCGCCAGAT 459
Qy 459 CAACATCCGATGCGACACTTGGCATGCGGTGCTGCGAGTGTGGAGCAGAGCTGTGGA 518
Db 460 GAATGCTAAGATGCTGCTTCCGACTCTTAATATGATGTCAGATGTGAATTTCTACG 519
Qy 519 GACCACTGTGTGCTCCCACTACGCTGCTCCGAGGTATCCGGGGGAGAGATGTA 578
Db 520 AACTAGCTGTGATGCGCAAAATATGACAGCCGAGGTATCTCAGGAAGCTGTATGC 579
Qy 579 CGGCGGAGAGCGAGCTGTGAGACTGCGGCTCATTCCTGTGCGCTGTGGTGGGCG 638
Db 580 GGGTCTGAGGTGATATCTGAGAGCTGTGTATCTGTATGCCCTTCTGTGACAC 639
Qy 639 TCTGCCCTTGCAGATGACAACTTGCAGACAGTGTGAGAGAGTGAAGCGGGCGTGT 698
Db 640 CTTCCCTGTGACATGAGAGAGAGCTGTGAGCTTAAAGAGATCCGAGGGGTGT 699
Qy 699 CCACATGCGCATTTTATCCCGCCGACGTGCAAGTGTGCTAAGGGGAGATGATGAGT 758

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Db 700 CTATATCCCGAGATCTCAACCGTTCTATTGCGACCTCTCATGTGACATGCTGAGGT 759  
 QY 759 GSAAGCGGCAAGCGGCTCAGCTAGAGACATTCAGAAACACATATGATATAGGG 817  
 Db 760 GGACCCCTTGAAGGACCACTATCAAGACATACAGAGCAAGATGTTTAAACGG 818

# RESULT 5 US-08-557-006C-24

; Sequence 24, Application US/08557006C  
 ; Patent No. 625847  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bert, Rajindar K.  
 ; APPLICANT: Carling, David  
 ; APPLICANT: Forster, Robert A.  
 ; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE  
 ; FILE REFERENCE: NGAP/PH37588/UST  
 ; CURRENT APPLICATION NUMBER: US/08/557, 006C  
 ; CURRENT FILING DATE: 1996-03-06  
 ; PRIOR APPLICATION NUMBER: PCT/GB94/01093  
 ; PRIOR FILING DATE: 1994-05-20  
 ; PRIOR APPLICATION NUMBER: GB 9310489.1  
 ; PRIOR FILING DATE: 1993-05-21  
 ; PRIOR APPLICATION NUMBER: GB 9318010.7  
 ; PRIOR FILING DATE: 1993-08-31  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: Patent Ver. 2.1  
 ; SEQ ID NO 24  
 ; LENGTH: 2761  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: cDNA of rat  
 ; OTHER INFORMATION: liver AMP protein kinase  
 ; US-08-557-006C-24

Query Match 11.2%; Score 225.4; DB 3; Length 2761;  
 Best Local Similarity 56.5%; Pred. No. 4.4e-42;

Matches 440; Conservative 0; Mismatches 336; Indels 3; Gaps 1;

QY 42 GATGTTGGGCTTACCGGCTGAGAGAGCGCTGGGCAAGGGGAGAGAGAGGTCTGTGAA 101  
 Db 56 GAAGATCGGACACTAGCTGCTGGGAGACACCTCGGCGTGGGACCTTGGCAAGTGA 115  
 QY 102 GCTGGGGGTTCACTGCGTCACTCGCAGAGGTGGCCATCAATGCTCAACCGTGA 161  
 Db 116 GATTGAGAAACATCAATTGACAGGCCATTAAGTGAAGTCTTAATTAAGACAGA 175  
 QY 162 GCTCAGCAGTCTGCTGATG---AAGTGAAGCGGAGATCGCATCTGAAGCTCAT 218  
 Db 176 GATTGCAAGTTAGTGTGTAAGAAATAAAGAGAAATCTTAACCTT 235  
 QY 219 TGAGCAACCCCACTCTTAAGTGCAGACGTTTATGAATAAATAATTTGACT 278  
 Db 236 TCGTCACTCTCAATTAATCAACTTACCAAGTACAGACTCCCAACGACTTTTAT 295  
 QY 279 GGTGCTAGAAACGTTGAGTGTGAGCTCTTCACTAGTGTGAAGAGGAGGT 338  
 Db 296 GGTAAATGAATATGTTCTGAGAGTGAATTTGTCGATCATCTGTAACAGGAGGT 355  
 QY 339 GACGCTTAAGAGGCTCGGAAGTTCTTCGGGAGATCATCTGCGCTGACTTCCCA 398  
 Db 356 TGAAGAGTGAAGCTGCGCGCTCTTCAGAGATCTGCTGCGCTGACTTCCCA 415  
 QY 399 CAGCCACTCATATGCGACAGGATGAAACCTGAAACCTTCGCTGGAAGAGAA 458  
 Db 416 CAGGCAATGTTGTTCAAGGAGCTGAAGCCAGAAAGTGTGCTGGAAGCCAGAT 475  
 QY 459 CAAATCCGATCGAGACTTTGGATGGCGTCCCTGAGGTTGGAGAGAGCTGTGA 518  
 Db 476 GAATGCTAAGATGAGTGAAGTCTGGAATCTTAATATGATGATGATGGAATTTCTAG 535

QY 519 GACGAGCTGTGGTCCCCCACTAGCCTGCCCGAGGTGATCCGGGGAGAAATGA 578  
 Db 536 AACTAGCTGTGATGCCAAATTAATGACAGACCGAGGTCACTTCAGAAAGCTGTAAGC 595  
 QY 579 CGGCGGAGAGGAGACGTTGAGAGTGGCGGTCACTCTTTCGCTTCTGTTGGGGC 638  
 Db 596 GGTCTTGAAGTGAATCTGGAAGTGTGTTATCTGATGCTCTTCTGTTGGGAC 655  
 QY 639 TCTGCCCTTCGACATGCAAACTTGCAGACAGTGTGAGAGGTAAGCGGGCGTGT 698  
 Db 656 CTTCCGTTTCAAGATGACAGCTGCTTACCTCTTTAAGAAATCCAGGGGTTGTT 715  
 QY 699 CCAATGCCGCACTTATCCCGCCGACTGCCAGAGTGTCTTACGGGCGATGATGAGT 758  
 Db 716 CTACATCCCGAGATCTCAACCGTTCTATTGCGACTTGTGATGACATGCTGACAGT 775  
 QY 759 GAGAGCGGCAAGCGGCTCAGCTAGAGACATTCAGAAACATATGATATAGGG 817  
 Db 776 GGACCCCTTGAAGGAGCACTATCAAGACATACAGAGCATGAATGTTTAAACAG 834

## RESULT 6

US-09-799-875-6  
 ; Sequence 6, Application US/09799875  
 ; Patent No. 6638721

; GENERAL INFORMATION:  
 ; APPLICANT: Meyers, Rachel  
 ; APPLICANT: Kapeller-Libermann, Rosana  
 ; APPLICANT: Williams, Mark  
 ; TITLE OF INVENTION: No. 6638721 Human Protein Kinases and Uses  
 ; FILE REFERENCE: 35800/208996  
 ; CURRENT APPLICATION NUMBER: US/09/799, 875  
 ; CURRENT FILING DATE: 2001-03-06  
 ; PRIOR APPLICATION NUMBER: 60/182,059  
 ; PRIOR FILING DATE: 2000-02-11  
 ; PRIOR APPLICATION NUMBER: 09/659,287  
 ; PRIOR FILING DATE: 2000-09-12  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 6  
 ; LENGTH: 3609  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-799-875-6

Query Match 10.7%; Score 214.6; DB 4; Length 3609;  
 Best Local Similarity 54.5%; Pred. No. 1.4e-39;  
 Matches 430; Conservative 0; Mismatches 359; Indels 0; Gaps 0;

QY 45 TGTGGGCGCTTACCGGCTGAGAGAGCTGGGCAAGGGGAGACAGTCTGTGAAGCT 104  
 Db 12 TATGCGCTACTAGAGATCGACCGCACATCGGCAAGGCACTTCGCGGTGTAAGCG 71  
 QY 105 GGGGTTTCACTGCTCACTGCGCAAGAGTGGCCATCAAGTCTCAACCGTGAAGCT 164  
 Db 72 GGCACGCACTCTCTCAACAGGCAAGGTTGCTATCAAGTCAATGATTAAGACCGACT 131  
 QY 165 CAGGAGTGGTGTGATGAAGTGGACCGGAGATGCGCATCTGTAAGTCAATTGAGA 224  
 Db 132 GATGAAGAAAATTGAAGAAATTTTCCGGGAAGTCAATATTAAGAAATGCTTGGCA 191  
 QY 225 CCCCCAGTCTCTAAGTGCAGAGCTTTATGAACAAATAATTTGATCTGAGTGT 284  
 Db 192 CCCCATATATATCAGGCTCTACAGGTTATGAGAGACAGAAAGATATTTATCTGAGT 251  
 QY 285 AGAACAGTGTCAAGTGTGAGTCTTCTGACTTCTGTGAAGAGAGGAGCTGAGCC 344  
 Db 252 AGAATATGCTAAGTGAAGGAGAAATATTTGAACAACCTGTGTGCGCCATGTAAGTGGAGA 311  
 QY 345 TAAAGAGGCTGGAAGTCTTCCGGCAGATCATCTGCGCTGAGCTTCTGCCACAGCA 404  
 Db 312 AAAGAGGCAAGTGGAGAGTTCAACAGATCTGACAGCTGTCTATTTTGTCTAGCTGT 371

QY 405 CTCATATGCCACAGGGATCTGAAACCTGTAACCTCTGTGACGAGAAACACAT 464  
 DB 372 GAACATGTTCAATCGATTAAAGCTGAAATTTACTTCTGATGCAATCTGAATAT 431  
 QY 465 CCGCATCGACACTTTGSCATGGCCCTCTGACAGTTGGCGACACCTGTTGAGACAG 524  
 DB 432 CAATAATGACAGATTTGTTTCACTTCTCACTCTGAGGACGCTGCTGAGACCTG 491  
 QY 525 CTGTGGGTCCCCCACTACGCTGCCCCAGGTGATCCGGGGGAGAAATATGACGCGC 584  
 DB 492 GTGTGGCAGCCCTCCCTATGCTGACCTGAACCTTTGAAGGAAATATGATGCGCC 551  
 QY 585 GAAAGCGGACGTGTGAGCTGGGGGCTCATCTGTTGCTGCTGCTGCTGGGGGCTCTCC 644  
 DB 552 CAAGGTGACATCTGAGGCTGAGGATTTCTCTACGCTGCTGCTGCTGCTGCTGCTG 611  
 QY 645 CTTCGACGATGACAACTTGGCAGCTGCTGAGAGGTGAAGCGGGGCTGTTCCAT 704  
 DB 612 ATTGATGAGAGACACTGCAAGATCTGGGGGCGCGCTGATGAGAAATTCGCGAT 671  
 QY 705 GCGGCACTTTATCCGCGCCGACTGCCAGCTCTGCTACGGGCGATGATGAGTGAAGC 764  
 DB 672 CCATTTTATGTTCCACAGATGTGAGCATTTGATCCGCAATATGTTGTTAGATCC 731  
 QY 765 CGACGCGGCTCAGCGTGAAGCATTCAGAAACATATGTTATAGGGGCGACAGA 824  
 DB 732 CAATTAAGCGCTCTCCATGAGGACATCTGCAAGCAAGTGAATGAACCTAGGGAGCC 791  
 QY 825 TGAGCCCGA 833  
 DB 792 CGATCCCAA 800

RESULT 7  
 US-09-799-875-4  
 ; Sequence 4, Application US/09799875  
 ; Patent No. 6638721

GENERAL INFORMATION:  
 APPLICANT: Meyers, Rachel  
 APPLICANT: Kapeller-Libermann, Rosana  
 APPLICANT: Williamson, Mark  
 TITLE OF INVENTION: No. 6638721e1 Human Protein Kinases and Uses  
 FILE REFERENCE: 35800/209996  
 CURRENT APPLICATION NUMBER: US/09/799,875  
 PRIOR FILING DATE: 2001-03-06  
 PRIOR APPLICATION NUMBER: 60/182,059  
 PRIOR FILING DATE: 2000-02-11  
 PRIOR APPLICATION NUMBER: 09/659,287  
 NUMBER OF SEQ ID NOS: 32  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 4  
 LENGTH: 5983  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (115)...(3723)  
 US-09-799-875-4

Query Match 10.7%; Score 214.6; DB 4; Length 5983;  
 Best Local Similarity 54.5%; Pred. No. 1.6e-39;  
 Matches 430; Conservative 0; Mismatches 359; Indels 0; Gaps 0;  
 QY 45 TGTGGGCGCCATCCGCGCTGAGAGACGCTGCGCAAGGGGCAAGAGTCTGTGAAGCT 104  
 DB 126 TATCGGCTACTACAGATGACCGGACCATCGGCAAGGGCAACTTCGCGTGTGCAAGC 185  
 QY 105 GGGGATTCAGTGCCTGACCTTGCCAGAAAGTGGCCATCAAGATCTCAACCGTGAAGCT 164  
 DB 186 GGGCAGCAGCTCTGACCAAGGCGCAAGGTTGCTATCAAGTCAATGATTAAGACCCAGCT 245

QY 165 CAGCGATGGTGTGATGAAAGTGGAGCGGAGATCGGATCTGAACTGATGAGCA 224  
 DB 246 GATTAAGAAACTTGAAGAGATTTCCGGAGAGTTCAATATGAAATGATGCTTGCCA 305  
 QY 225 CCCCACGCTCTAAAGCTGACGACCTTTATGAAAACAAAAATATTTGTACTGTGCT 284  
 DB 306 CCCCATATCATCAGCTCTACCCAGGTTATGAGACAGACGAGATTTATCTGTGAC 365  
 QY 285 AGAACACGTCTAGGTGGTGTAGCTCTGACCTGCTGTAAGAAAGGAGGCTGACGCC 344  
 DB 366 AGAATATGCTAGTGAAGGGGAAATATTTGACCACTGCTGGCCCATGATGACAGA 425  
 QY 345 TAAGAGCTCGGAAGTCTTCGCGAATCATCTGCGCTGAGATTCTGCCACAGCCA 404  
 DB 426 AAGAGGCGACGTGCGAAGTTCAACAGATCGTCAAGCTGTCTATTTTGTACTGTGC 485  
 QY 405 CTCATATGACACAGGATCTGAAACCTGAAACCTCTGCTGGAAGAGAAACAAT 464  
 DB 486 GAACATTTGTCATGATTTAAAGCTGAAATTTACTTCTGATGCCAATCTGAATAT 545  
 QY 465 CCGCATCGACACTTTGGCATGGCTCTCCCTGACAGTTGGGACAGCCTGTTGAGACCA 524  
 DB 546 CAATAATGACAGATTTTGTGTTTCAAGTAACTCTTCACTCTGCGGACGCTGTAAGACT 605  
 QY 525 CTGTGGTCCCCCACTACGCTGCCCCGAGGTGATCCGGGGGAGAAATGACGCGC 584  
 DB 606 GTGTGGCAGCCCTCCCTATGCTGACCTGAACTTTTGAAGAAATATATATGAGCC 665  
 QY 585 GAAAGCGGACGTGTGAGAGCTGCGCGCTGCTCTGCTGCTGCTGCTGCTGCTGCTG 644  
 DB 666 CAATGAGACATCTGAGAGCTTGGAGTTGCTCTGAGTCTTGTGAGGCTGCCCTGCC 725  
 QY 645 CTTCGACGATGACAACTTGGCAAGCTGCTGAGAAAGTGAACGGGGCTGTTCCAT 704  
 DB 726 ATTGATGAGAGCACATGCAAGATCTGCGGGCGCGCTGATGAGAAAGTTCCGAT 785  
 QY 705 GCGCCACTTTATCCGCGCCGACTGCCAGCTGCTGCTACGGGCGATGATCAGGTGAGC 764  
 DB 786 CCATTTTATGTTCCACAGATGTGAGCATTTGATCCGCAATGTTGTTAGATCC 845  
 QY 765 CGCAGCGGCTCAGCTGAGGACATTCAGAAACATATGTTATGAGGGGCAAGAA 824  
 DB 846 CAATTAAGCGCTCTCCATGAGGACGATCTCAAGCAAGTGAATGAAGCTAGGGAGCC 905  
 QY 825 TGAGCCCGA 833  
 DB 906 CGATCCCAA 914

RESULT 8

US-09-930-181-5  
 ; Sequence 5, Application US/09930181  
 ; Patent No. 6455292  
 GENERAL INFORMATION:  
 APPLICANT: Origene Technologies  
 TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas  
 FILE REFERENCE: 16U 101 VI  
 CURRENT APPLICATION NUMBER: US/09/930,181  
 PRIOR FILING DATE: 2001-08-16  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 5  
 LENGTH: 213  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)...(213)  
 US-09-930-181-5

Query Match 10.6%; Score 213; DB 4; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-39;  
 QY 105 GGGGATTCAGTGCCTGACCTTGCCAGAAAGTGGCCATCAAGATCTCAACCGTGAAGCT 164  
 DB 186 GGGCAGCAGCTCTGACCAAGGCGCAAGGTTGCTATCAAGTCAATGATTAAGACCCAGCT 245

Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACATGACGGGGAGAGAGCGGGCGCCAGACGCGAGTATGTTGGCCCTACCG 60  
Db 1 ATGACATGACGGGGAGAGAGCGGGCGCCAGACGCGAGTATGTTGGCCCTACCG 60  
QY 61 CTGAGAGAGCGCTGGGCGAAGGGGCGAGAGGTCTGTGAAGCTGGGGGTTCACTGCGTC 120  
Db 61 CTGAGAGAGCGCTGGGCGAAGGGGCGAGAGGTCTGTGAAGCTGGGGGTTCACTGCGTC 120  
QY 121 ACCGCGAGAGGTGCGCATCATAGATCGTCAACCGTGAAGCTCAAGCGAGTGGTCTG 180  
Db 121 ACCGCGAGAGGTGCGCATCATAGATCGTCAACCGTGAAGCTCAAGCGAGTGGTCTG 180  
QY 181 ATGAAGGTGAGCGGGAGATCGCGATCTCTGAAG 213  
Db 181 ATGAAGGTGAGCGGGAGATCGCGATCTCTGAAG 213

## RESULT 9

US-09-101-146-44  
Sequence 44; Application US/09101146  
Patent No. 6124125  
GENERAL INFORMATION:  
APPLICANT: Dartmouth College, St. Vincent's Institute of  
APPLICANT: Medical Research, Kemp et al.  
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PC  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/101,146  
FILING DATE: October 7, 1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PNT450  
FILING DATE: 8 JAN 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: DC-0050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (856) 810-1515  
TELEFAX: (856) 810-1454  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1647  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: No  
US-09-101-146-44

Query Match 10.6%; Score 213; DB 3; Length 1647;  
Best Local Similarity 55.6%; Pred. No. 2.5e-39;  
Matches 430; Conservative 0; Mismatches 340; Indels 3; Gaps 1;

QY 42 GTATGTTGGGCGCTACCGGTGAGAGCGCTGGGCGAAGGGGCGAAGAGTCTGTGA 101  
Db 33 GAGAGTCGCGACATACCTCTGGGGAGACGCTGGGCGAAGGGGCGAAGAGTCTGTGA 92  
QY 102 GCTGGGGGTTCACTGCTGCTACCTGCGAGAGAGTGGCATCAAGATGTCACCGTGA 161

Db 93 GGTGGCGAAGCAGAGTGTGACTGACATTAAGTTGCTGTGAAGTACTCAACGGCAGAA 152

QY 162 GCTC--AGCGAGTGGTGTGATGAGAGTGGAGCGGAGATCGCATCTGAAGCTCAT 218  
Db 153 GATTGAGAGCGTGAAGTGTGCGGAGAAATCCGAGAGATTCAGAACTGAAAGCTTTT 212

QY 219 TGAGACACCCCGACGCTCTTAAGTGTGACAGAGTGTATGAACAAATAATTTGTACT 278  
Db 213 CAGGACACCTCATATTAACAACTGTACAGTCAACAGTCAACCGTGTATATTTTCA 272

QY 279 GGTGTAGAACCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 338  
Db 273 GGTGTAGAACCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 332

QY 339 GACGCTTAAGAGGCTGGAAAGTTCTTCCGAGATCATCTGTGCTGAGACTTCTGCA 398  
Db 333 GACGCTTAAGAGGCTGGAAAGTTCTTCCGAGATCATCTGTGCTGAGACTTCTGCA 392

QY 399 CAGCCATCCATATGCGCACAGGATCTGAACCTGAAACCTGCTGCGAGAGAA 458  
Db 393 CAGCCATATGCTGTCCACAGATTTGAACCTGAAACCTGCTGCGAGAGAA 452

QY 459 CAACATCCGACATCGCAGACTTTGGCATGCGCTCCCTGCGAGTGGCGACAGCTGTGA 518  
Db 453 GAATCAAAAGATGAGCGAGCTTCCGCTTCAACATGATGTCAGATGGTGAATTTTAA 512

QY 519 GACCAAGTGTGGTCTCCCGCACTACGCTGCGCGAGTGTATCCGGGGGAGAAATGA 578  
Db 513 AACGAGCTGTGGCTCGCCCAATATGTCACACGAGAAATATTCAGAAAGATTTCA 572

QY 579 CGGCGGAGAGCGGACGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 638  
Db 573 AGGCGCTGAATGAGCATCTGAGAGAGGGGTCTATCTATGCTTGTGCTGTGAGAC 632

QY 639 TCTGCTTTCAGATGACAACTTGGCAGACCTGCTGAGAGTGAACCGGGCGTGT 698  
Db 633 TCTGCTTTCAGATGACAACTTGGCAGACCTTTCAGAGAGATGTCAGAGGATAT 692

QY 699 CCACATGCGGACCTTATCCCGCCGACCTGCGAGAGTGTGAGGCGGATGACAGT 758  
Db 693 TTATGCTTTCAGATGACAACTTGGCAGACCTTTCAGAGAGATGTCAGAGGAT 752

QY 759 GAGCGCGGACGCGCTCAAGCTAGAGCAGATTCAGAAACATATGATATA 811  
Db 753 AGATCTTATGAAGAGGCGCAATATAAAGATATGAGGAGATGATATGATATA 805

## RESULT 10

US-09-984-890-1  
Sequence 1; Application US/09984890  
Patent No. 6492156  
GENERAL INFORMATION:  
APPLICANT: YAN Chunhua et al.  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: C1001306  
CURRENT APPLICATION NUMBER: US/09/984, 890  
CURRENT FILING DATE: 2001-10-31  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2175  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-984-890-1

Query Match 10.6%; Score 212.6; DB 4; Length 2175;  
Best Local Similarity 54.2%; Pred. No. 3.4e-39;  
Matches 431; Conservative 0; Mismatches 354; Indels 0; Gaps 0;

QY 47 TTGGGCGCTTACCGGTGAGAGAGTGTGGCGAAGGGGCGAGACAGTCTGTGTAAGCTGG 106

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Db      149 TTGAAACTACCGGCTCTCTCAAGACCATTTGGCAAGGTAAATTTTCCAGGTGAAGTTGG 208
Qy      107 GGGTTCACGTGGGTCACCTGCGCAGAGGTGGCCATCAATGCTCAACCTGAGAGTCA 156
Db      209 CCGGACACATCTCTGACTGGAAAGAGGTAGCTGTGAAGATTAATGACAAGACTCACTGA 258
Qy      167 GCGAGTGGGTGTGTAAGAGGTGAGCGGAGATCGCATCTGAAGCTCATTTGAGCACC 226
Db      269 ACTCCCTCCAGCTCCAGAAACTATTTCCCGAGAGTAAATATGAGGTTTGAATCATC 328
Qy      227 CCCAGCTCTAAAGCTGACGACGCTTTTGAACAAATAAATTTTCTACTGGTGTAG 286
Db      329 CCAACTAGTTAAATTAATTTTGAAGTATGAGATGAGAAACCTCTACTGTCATGG 388
Qy      287 AACAGCTGACGTGTGTGATCTTCTGACATCTGCTGTGAAGAGGAGGCTGACCGCTA 346
Db      389 AGTAGGCTAGTGGCGGAGAGGTATTTGATTAAGTGTGCTGACAGATGAAGAAA 448
Qy      347 AGAGGCTCGAAGTTCTTCCGCGAGATCATCTCGGCGTGGACTTGTGCGACAGCAGT 406
Db      449 AAGAGGCTGAGCCAAATTCGCGAGAGTGTGTCTGCTGCACTGTCAACAGAGT 508
Qy      407 CCATATGCCACAGGAGATCTGAACCTGAAACCTCTGTGAGCAGAGAGACAGATCC 466
Db      509 TTATGTCCATAGAGACTTAAAGCAGAAACCTGCTTGAATGCTGATATGAACATCA 568
Qy      467 GCATGCGACATTTGGCATGGGCTCCCTGACAGTTGGCGACAGCTGTGGAAGACAGT 526
Db      569 AATTTGCAAGCTTTGGCTTTCAGCATGATTAATCACTTTGGGAACAGCTGACACTTCT 628
Qy      527 GTGGTCCCCCACTACGCTGCGCCGAGGTATCGGGGGGAGAGATGACGGCCGGA 586
Db      629 GTGGAGTCCCCCTTATCTGCCCCAGAACTTTCAGGGCAAAAATATGATGAGACCG 688
Qy      587 AGCGGACGCTGTGAGCTGCGGCGCATCTGCTGCGCTGTGCTGGGGCTCTGCTCCT 646
Db      689 AGGTGAGTGTGAGCTGTGAGATTAATCTCTTAACATGCTGACGGAATCCCTGCTT 748
Qy      647 TCGAGATGACACTTGGCAGAGCTGCTGAGAAAGTGAACGCGGGCGTTCACATGC 706
Db      749 TTGATGAGACAGAACTCAAGAGAGCTGCGGGAACGGGTATGAGGGGAAAATACCTATTC 808
Qy      707 GCACATTTATCCCGCGGAGCTGCGAGAGTCTGCTAGGGGCAATGATCGAGGTGAGACCG 766
Db      809 CATTTAATGTCCACGAGCTGTGAAAACCTGCTTAAATAATTTCTATTTTAAATCCA 868
Qy      767 CACGCGGCTTACGCTAGAGCACTTGAAGAAACATATGATATAGGGGCGCAGATG 826
Db      869 GCAAGAGAGGCACTTGAAGCAATCATGAAGATGATGATGATGATGATGATGATGATG 928
Qy      827 AGCCGGAACGAGAGC 841
Db      929 ATGATGAATTAAGC 943

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; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 44
; LENGTH: 1747
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: gene
; LOCATION: (1) ..(1747)
; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
; OTHER INFORMATION: nucleotide 1765
US-08-557-006C-44

Query Match      10.0%; Score 200.4; DB 3; Length 1747;
Best Local Similarity 56.1%; Pred. No. 1.9e-36;
Matches 440; Conservative 0; Mismatches 336; Indels 8; Gaps 3;

Qy      42 GTATGTTGGGCGCTACCGGCTGAGAGAACCGTGGGCAAGGGCGACAGCTGTGTGA 101
Db      33 GAAATGCGACACTGCTGCTGGGAGACCTCTGGCGTGGCACTTGGCAAAAGTGA 92
Qy      102 GCTGGGGGTTCACTGCTCACTGCGAGAGGTGGCATCAAGATGCTCAACCTGAGAA 161
Db      93 GATTGGAACATCAATTGACAGGCCATAAAGTGGCAGTTAAGATCTTAAATGACAGAA 152
Qy      162 GCTGAGGAGTCCGTGTGATG--AAGTGGAGCGGAGATCGCATCTGAAGCTCAT 218
Db      153 GATTGCGAGTTTGAATGTTGTGAAATAAATGAAGAAATTCAAATCTTAACTCTT 212
Qy      219 TGAGCACCCCACTGCTTAAGCTGACAGACGTTTATGAAAAAATAATTTGTACT 278
Db      213 TCGCATCTCATATTAATTAACCTTACCAAGATGATCAGATCCCAAGACATTTTAT 272
Qy      279 GGTCTGAACACAGCTGAGGTGTGAGCTCTTCACTCTGCTGTGAGAAAGGAGGCT 338
Db      273 GGTATGAAATATGTGTGAGAGTGAATTTGTGACTAATCTGTAACAGGAGGAT 332
Qy      339 GACGCTTAAGAGAGCTGGAAGTTCTTCCGAGATCATCTGTGCGTGAATCTTG--C 396
Db      333 TGAAGAGGTGAAGCTGCGCGGCTTTCAGCAGATTTGTCTGCGTGTGACTGTCT 392
Qy      397 CAGAGGACCTCCATATGCGACAGGATCTGAAACCTGAAACCTCTCTGTGAGAGAG 456
Db      393 CAGAGGACATGTTGTGCAAGGAGCTGAAGCCAGAGAAAGTGTGCGAGCCGAG 452
Qy      457 AACAACTCCGATCCGACATTTGGCATGAGCGCTCCCTGACAGTTGGGAGACAGCTGTG 516
Db      453 ATGATGCTTAAGATAGCTGACTCGACTCTTAATATGATGATGATGATGATGATGATG 512
Qy      517 GAGACGAGCTGTGGGTCCCCCACTACGCTGCTCCGAGGTATCCGGGGGAGAGAT 576
Db      513 GAACTAGCTGTGATGCGCAATTAATGAGACCGGAGGTATTCAGAAAGGCTGTAT 572
Qy      577 GACGGCGGAAGCGGAGCTGTGAGAGCTGCGGCTCATCTGTTGCGCTTGTGGTGGG 636
Db      573 GCGGCTCTGAGGTGATTAATCTGAGCTGTGTATTCCTGTATGAGCCCTCTGTGCTG 632
Qy      637 GCTTGTGCTT---GAGATGACAACTTGGCAGAGCTGTGAGAAAGTGAAGCGGGG 693
Db      633 ACCCTCCGTTGACAGACATAGACGCTGCTACGCTCTTAAAGAAATCCGAGGGGT 692
Qy      694 GTGTTCAACATGCGGCACTTTATCCCGCGGCACTGCGAGATGCTGCTGAGGAGATGTC 753
Db      693 GTGTTCAACATCCCGAGATATCAACGCTTATATGCACTCTGATGACATGCTG 752
Qy      754 GAGGTGAGACCGGACGCGGCTGACGCTAGAGCACTTCAAGAAACATATGATGATTA 813
Db      753 CAGGTGAGCCCTTGAAGGAGCACTATCAAGACATACAGAGACATGAATGTTTAA 812
Qy      814 GGGG 817
Db      813 CAGG 816

```

## RESULT 12

US-09-359-161-4

Sequence 4, Application US/09359161A

Patent No. 6342656

GENERAL INFORMATION:

APPLICANT: Bradford, Kent J.

APPLICANT: Danal, Peetambar

APPLICANT: Yang, Hong

APPLICANT: Cooley, Michael

APPLICANT: Domier, Bruce

APPLICANT: Gee, Oliver

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses

FILE REFERENCE: 023070-095900US

CURRENT APPLICATION NUMBER: US/09/359,161A

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 1929

TYPE: DNA

ORGANISM: Lycopersicon esculentum

FEATURE:

OTHER INFORMATION: Lycopersicon esculentum plant homolog of yeast

OTHER INFORMATION: SNF1 kinase subunit of protein kinase (lesnfl)

US-09-359-161-4

Query Match: 9.5%; Score 191.4; DB 4; Length 1929;

Best Local Similarity 54.0%; Pred. No. 2.2e-34;

Matches 415; Conservative 0; Mismatches 351; Indels 3; Gaps 1;

QY 43 TATGTGGGCCCTACCGGCTGAGAGACGCTGAGGAGGCGACAGCTCTGTGAAG 102

DB 75 TTTTACGGAACTATAAATCGGGAAACACTTGGATTGGATCGTCCGAAAGTTAA 134

QY 103 CTGGGGGTTACGTCGCTCACTCCGAGAGGTGGCCATCAAGTCGTCAACCTGGAAG 162

DB 135 ATAGCTGAACATCGTTAACAGGCAACAAAGTCTGTCAAGTCTTAATCGTCAAAA 194

QY 163 CTCAGGAGTCG---TGCTGATGAAGTGAAGCGGAGATCGCATCCGTAAGTCATT 219

DB 195 ATAGGAATATGACATGAGAGAAAGTCCGTAGAAATCAAAATATTGAGATTGTC 254

QY 220 GACGACCCCAAGCTCTAAAGCTGACGACGCTTATGAAAACAAAATATTTGTA 279

DB 255 ATGATCTCTCATATTAATACGGCTTATGAGTCAATAGACACATCAGATATATGTT 314

QY 280 GTGCTAGAACACGTCGAGTGTGAGCTCTTGACATCGTGTGAAGGGGAGGCTG 339

DB 315 GTATGAGATATGTAATTCGCGAGTTATTTGATTAATGTTGAGAAAGGCAATG 374

QY 340 AGCCCTAAGAGGCTCGAAGTTCTTCGCGACATCATCTGCGTGAATCTTCCAC 399

DB 375 CAGAGGATGAAGCTGTAACTTTTTCAGAGATATTTCTGGGTGAGATGCGCAT 434

QY 400 AGCCATCCATATGCGACAGGATCTGAAACCTGAAAACCTCTGCTGACGAGAAAC 459

DB 435 AGAAACATGCTGTTCAATAGACCTTAAAGCTGAAAACCTCTTGTGACCTCCAAATG 494

QY 460 AACATCCGATCGACAGCTTTGACATGCGTCCCTGACAGTTGGACAGCTGTGGAG 519

DB 495 AATGTGAATGCAATTTTGGTTTGAAGCAATATATGCGGATGCTATTTTCTGAAG 554

QY 520 AACAGCTGTGGTCCCCCACTAGGCTGCGCCGAGGTATCCGGGGGAGAAATATGAC 579

DB 555 ACAAGTTGCGAAGCCCAATATATGCTGCGCCAGAGTATATCAAGTAAATGTATGCT 614

QY 580 GGCAGGAGGCGAGCTGTGAGCTGCGGCTCATCTGTGCGCTTGTGAGGGGCT 639

DB 615 GGCCTGAGGTATATGAGCTGTGTTATCTTATGCTCTTCTGTGACAC 674

## RESULT 13

US-09-579-664B-4

Sequence 4, Application US/09579664B

Patent No. 6514719

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Bird, Timothy A.

APPLICANT: Virca, G. Duke

APPLICANT: Martin, Unja

APPLICANT: Anderson, Dirk M.

TITLE OF INVENTION: NOVEL MORINE AND HUMAN KINASES

FILE REFERENCE: 2923-A

CURRENT APPLICATION NUMBER: US/09/579,664B

NUMBER OF SEQ ID NOS: 36

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 2902

TYPE: DNA

ORGANISM: Mus musculus

US-09-579-664B-4

Query Match: 9.3%; Score 186.4; DB 4; Length 2902;

Best Local Similarity 53.5%; Pred. No. 3.4e-33;

Matches 413; Conservative 0; Mismatches 356; Indels 3; Gaps 1;

QY 52 CCTACCCGCTGAGAAAGCCTGGCAAGGAGGAGACAGAGTCTGTGAAGCTGGGGT 111

DB 288 CGCTACGAGTTCCTGAGAACCTGGCAAGGCACTGAGGAGTTGAAGGACACGA 347

QY 112 CACTGCGTACCTGCGAAGGTGGCATCAAGTCGTCAACCTGAGAGCTGACGAG 171

DB 348 GAGAGCTGGGGCGTCTGTGGTCCATCAAGTCCATCAGAAAGCAAAATCAAGATGAG 407

QY 172 TCGGTGCTGATGAAGGTGAGACGGAGATCGCATCCGTAAGTCATTGAGACCCCCAC 231

DB 408 CAGATCTGCTGACATACGAGAGGAGATTGAGATCATGTTTACTCAACACCCCCAC 467

QY 232 GTCTAAAGCTGACAGCGTTATGAAAACAAAATATTTGTAACCTGTGCTGAACAC 291

DB 468 ATCATTTGCCATCATGAAGTTTGAAGATGACAGCAAGATTGATGTCATGAGATAT 527

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DB 528 GCGAGCCGAGATCTGATATTAATCAATGAGGCGCAAGCTGATGAGCGGAC 587

QY 352 GCTCGAAGTCTTCGCGACATCATCTGCGCTGACATTTCTGCGACAGCTCATCATA 411

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QY 412 TGCCACAGGATCTGAAACCTGAAACCTCTGCTGTAAGGAGAAACATATCCATC 471

DB 648 GTTACCGAGATCTCAAGCTGGAACATCTTCTTATGCAATGCAATGCAATCAATG 707

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Db      888 GGGCAGGATCATTAACAACACTGTGTGAAGCAATCACTGTAACGGGGCTTACCGTGAAGCGGCC 947
Oy      712 TTATTCGCGCCCACTGCGACAGTGTCTGTAAGGAGCAATGATCGAGTGAAGCGCGACGC 771
Db      948 ---AAGCGTCCGATGCTGTGGCTGATCCGGTGGCTGTATGATGTAAGCCGACCCGCT 1004
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## RESULT 14

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US-08-557-006C-37
; Sequence 37, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carlings, David
; APPLICANT: Forde, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM7588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent Ver. 2.1
; LENGTH: 1736
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat liver AMP
; US-08-557-006C-37

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Query Match      8.8%; Score 176.6; DB 3; Length 1736;
Best Local Similarity 52.6%; Pred. No. 4.9e-31;
Matches 408; Conservative 0; Mismatches 364; Indels 3; Gaps 1;

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## RESULT 15

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US-08-557-006C-36
; Sequence 36, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajindar K.
; APPLICANT: Carlings, David
; APPLICANT: Forde, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHM7588/UST
; CURRENT APPLICATION NUMBER: US/08/557,006C
; CURRENT FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1783
; TYPE: DNA
; ORGANISM: Human AMP protein kinase
; US-08-557-006C-36

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Query Match      8.8%; Score 176.6; DB 3; Length 1783;
Best Local Similarity 52.6%; Pred. No. 4.9e-31;
Matches 408; Conservative 0; Mismatches 364; Indels 3; Gaps 1;

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2004, 08:35:27 ; Search time 657 Seconds

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	2007	100.0	2007	14	US-10-054-579-1	Sequence 1, Appli
2	2005.4	99.9	2908	15	US-10-195-072-1	Sequence 1, Appli
3	2005.4	99.9	2908	15	US-10-195-071-1	Sequence 1, Appli
4	1993	99.3	3364	15	US-10-195-072-3	Sequence 3, Appli
5	1993	99.3	3364	15	US-10-195-071-3	Sequence 3, Appli
6	1966	98.0	2647	13	US-10-362-892-42	Sequence 42, Appli
7	1966	98.0	2647	16	US-10-288-798-42	Sequence 42, Appli
8	1941.2	96.7	2025	15	US-10-283-247-1	Sequence 1, Appli
9	1939.6	96.6	2025	9	US-09-842-582-3	Sequence 3, Appli
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12	1777.4	88.6	3791	13	US-10-425-114-26842	Sequence 26842, A
13	1685.2	84.0	1911	15	US-10-283-247-4	Sequence 4, Appli
14	965	48.1	2337	13	US-10-423-543-12	Sequence 12, Appli

15	965	48.1	2337	15	US-10-116-326-1	Sequence 1, Appli
16	965	48.1	2980	13	US-10-423-543-10	Sequence 10, Appli
17	965	48.1	2980	15	US-10-354-358-91	Sequence 91, Appli
18	964.4	48.1	2897	17	US-10-311-034-43	Sequence 43, Appli
19	851.4	42.4	2112	15	US-10-116-326-5	Sequence 5, Appli
20	777.2	38.7	2269	15	US-10-116-326-3	Sequence 3, Appli
21	594	29.6	2173	15	US-10-102-558-1	Sequence 1, Appli
22	594	29.6	2173	15	US-10-102-558-1	Sequence 1, Appli
23	588.8	29.3	1797	16	US-10-120-988-221	Sequence 221, App
24	449.2	22.4	906	13	US-10-276-774-72	Sequence 72, Appli
25	409.8	20.4	1949	13	US-10-425-114-26847	Sequence 26847, A
26	291.6	14.5	512	9	US-09-960-253-87	Sequence 87, Appli
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29	265	13.2	1594	15	US-10-284-060-3	Sequence 3, Appli
30	264.2	13.2	1549	13	US-10-016-248-23	Sequence 23, Appli
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33	264.2	13.2	2462	13	US-10-363-616-158	Sequence 158, App
34	264.2	13.2	3226	15	US-10-161-565-23	Sequence 23, Appli
35	264.2	13.2	3269	16	US-10-258-106-34	Sequence 34, Appli
36	264.2	13.2	3312	17	US-10-276-645-3	Sequence 3, Appli
37	264.2	13.2	3392	17	US-10-276-645-4	Sequence 4, Appli
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39	264.2	13.2	4917	15	US-10-161-565-22	Sequence 22, Appli
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## ALIGNMENTS

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US-10-054-579-1
; Sequence 1, Application US/10054579
; Publication No. US20020137913A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020137913A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0300-USA
; CURRENT APPLICATION NUMBER: US/10/054,579
; PRIOR APPLICATION NUMBER: 2002-01-22
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-579-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2007; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 ; FILE REFERENCE: 16U 101 C2  
 ; CURRENT APPLICATION NUMBER: US/10/195,072  
 ; CURRENT FILING DATE: 2002-07-15  
 ; PRIOR APPLICATION NUMBER: US 09/930,181  
 ; PRIOR FILING DATE: 2001-08-16  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: Patentin Version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 2908  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (106)..(2112)

## OTHER INFORMATION:

US-10-195-072-1

Query Match 99.9%; Score 2005.4; DB 15; Length 2908;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2006; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGACATCGAGCGGGGAGAGAGCGCGCGCGCGAGCAGCCGCGAGTATGTTGGGCGCTTACCGG 60  
 DB 106 ATGACATCGAGCGGGGAGAGAGCGCGCGCGCGAGCAGCCGCGAGTATGTTGGGCGCTTACCGG 165  
 QY 61 CTGAGAGAGAGCGCTGGGCGAGGGGCGAGCAGGTCTGGTGAAGCTGGGGGTTTCACTGGCTC 120  
 DB 166 CTGAGAGAGAGCGCTGGGCGAGGGGCGAGCAGGTCTGGTGAAGCTGGGGGTTTCACTGGCTC 225  
 QY 121 ACCCGCAGAGAGGTGGCCATCAAGATCGTCAACCGGTAGAAGCTCAGCGAGTGGTCTG 180  
 DB 226 ACCCGCAGAGAGGTGGCCATCAAGATCGTCAACCGGTAGAAGCTCAGCGAGTGGTCTG 285  
 QY 181 ATGAGGTGAGAGCGGGAGATCGCGATCTGTAAGCTATTGAGCAGCCCGCGCTTAAAG 240  
 DB 286 ATGAGGTGAGAGCGGGAGATCGCGATCTGTAAGCTATTGAGCAGCCCGCGCTTAAAG 345  
 QY 241 CTGACAGCAGTTTATGAAAAAATAATTTTATCTGGTGTGTAAGACAGTGTCAAGT 300  
 DB 346 CTGACAGCAGTTTATGAAAAAATAATTTTATCTGGTGTGTAAGACAGTGTCAAGT 405  
 QY 301 GGTAGCTCTTTCAGCTACCTGTGTGAAGAGGGAGGCTGACGCTTAAAGAGGCTCGAGAG 360  
 DB 406 GGTAGCTCTTTCAGCTACCTGTGTGAAGAGGGAGGCTGACGCTTAAAGAGGCTCGAGAG 465  
 QY 361 TTCTTCCGGCAGATCATCTCTGCGCTGACCTTTCGCGACGCCACTCATATATGCGACAG 420  
 DB 466 TTCTTCCGGCAGATCATCTCTGCGCTGACCTTTCGCGACGCCACTCATATATGCGACAG 525  
 QY 421 GATGTAAACCTGTAACCTCTCTGCTGAGCAGAGAGAAACAATCCGATCGAGACTTT 480  
 DB 526 GATGTAAACCTGTAACCTCTCTGCTGAGCAGAGAGAAACAATCCGATCGAGACTTT 585  
 QY 481 GGCATGCGCTTCCCTGAGGTGGGAGAGCCTGTTGAGACAGCTGTGGTCTCCCGCAC 540  
 DB 586 GGCATGCGCTTCCCTGAGGTGGGAGAGCCTGTTGAGACAGCTGTGGTCTCCCGCAC 645  
 QY 541 TACGCTGCGCCGAGGTGATCCGGGGGAGAGATGATGACGCGGAGGCGAGCGTGTG 600  
 DB 646 TACGCTGCGCCGAGGTGATCCGGGGGAGAGATGATGACGCGGAGGCGAGCGTGTG 705  
 QY 601 AGCTGCGCGCTCATCTCTGCTTCTGCTGTGGGGGCTCTGCCCTTCAAGATGACAC 660  
 DB 706 AGCTGCGCGCTCATCTCTGCTTCTGCTGTGGGGGCTCTGCCCTTCAAGATGACAC 765  
 QY 661 TTGCGAGAGCTGTGAGAGAGTGAAGCGGGGCGTGTTCACATGCGCGCACTTATCCG 720  
 DB 766 TTGCGAGAGCTGTGAGAGAGTGAAGCGGGGCGTGTTCACATGCGCGCACTTATCCG 825  
 QY 721 CCGCATGCGCAGAGTCTGCTACGGGGCATGATGAGGTGACGCGCGACGCGCTTACG 780  
 DB 826 CCGCATGCGCAGAGTCTGCTACGGGGCATGATGAGGTGACGCGCGACGCGCTTACG 885  
 QY 781 CTAGAGCAGTTGAGAAACATATGATATATAGGGGGCAAGATGAGCCCGAACAAG 840  
 DB 886 CTAGAGCAGTTGAGAAACATATGATATATAGGGGGCAAGATGAGCCCGAACAAG 945  
 QY 841 CAGCCCATCTTCGCAAGGTGAGATCGCTCGTGCACAGCTGAGAGACATGACCC 900  
 DB 946 CAGCCCATCTTCGCAAGGTGAGATCGCTCGTGCACAGCTGAGAGACATGACCC 1005  
 QY 901 GAGCTGCTGAGCAGAGTGAATGCACTGAGGCTGCTCGAGACGCGCAACAAGCTGCGAG 960  
 DB 1006 GAGCTGCTGAGCAGAGTGAATGCACTGAGGCTGCTCGAGACGCGCAACAAGCTGCGAG 1065  
 QY 961 GACCTGCTGCTCGAGAGAGAACAGAGAGATGATTTACTTCTCTCTGAGACCGG 1020

DB 1066 GACCTGCTGCTCGAGAGAGAACAGAGAGATGATTTACTTCTCTCTGAGACCGG 1125  
 QY 1021 AAGAGAGGTACCCGAGCCAGAGAGATGAGACCTGCCCGCCGAGACAGATAGACCT 1080  
 DB 1126 AAGAGAGGTACCCGAGCCAGAGAGATGAGACCTGCCCGCCGAGACAGATAGACCT 1185  
 QY 1081 CCCCCGAGAGCTGTGATCTCCCCGATGCTGAAACCGGACAGGACAGCGCGCGCAGAACGC 1140  
 DB 1186 CCCCCGAGAGCTGTGATCTCCCCGATGCTGAAACCGGACAGGACAGCGCGCGCAGAACGC 1245  
 QY 1141 AATCCATGAGAGTGTCTCAGCGTGAAGCAGCGCGGCTCCCGGCTCTGCGCGCGGCG 1200  
 DB 1246 AATCCATGAGAGTGTCTCAGCGTGAAGCAGCGCGGCTCCCGGCTCTGCGCGCGGCG 1305  
 QY 1201 ATTGAGATGGCCACAGCAGGCGCAGAGGTCTCGTCCATCAGCGGTGCTCTCAGGCTT 1260  
 DB 1306 ATTGAGATGGCCACAGCAGGCGCAGAGGTCTCGTCCATCAGCGGTGCTCTCAGGCTT 1365  
 QY 1261 TCACACAGCCACTCAGCAGCGCCCGGGTGAACCCCTCAACCCCTCAACAGGGGCGAGTCC 1320  
 DB 1366 TCACACAGCCACTCAGCAGCGCCCGGGTGAACCCCTCAACCCCTCAACAGGGGCGAGTCC 1425  
 QY 1321 CTCCCGACCCCGAGGGGACACTGTGCAACGCCAAAGAGAGCCCGGCTGACGCGCC 1380  
 DB 1426 CTCCCGACCCCGAGGGGACACTGTGCAACGCCAAAGAGAGCCCGGCTGACGCGCC 1485  
 QY 1381 AACCCACGCCCCCGTCCAGCCCGCGCGAGGGGTCCCTGAGAGGGCGCGGCTCAAC 1440  
 DB 1486 AACCCACGCCCCCGTCCAGCCCGCGCGAGGGGTCCCTGAGAGGGCGCGGCTCAAC 1545  
 QY 1441 TCCATCAAGAACAGCTTCTGAGGCTCACCCGCTTCAACCGCGGAAACTGCAAGTTCCG 1500  
 DB 1546 TCCATCAAGAACAGCTTCTGAGGCTCACCCGCTTCAACCGCGGAAACTGCAAGTTCCG 1605  
 QY 1501 AGCGGAGAGATGCTCAACTGACACCGAGTGTCTCCAGAGCTGGCGAAGATTC 1560  
 DB 1606 AGCGGAGAGATGCTCAACTGACACCGAGTGTCTCCAGAGCTGGCGAAGATTC 1665  
 QY 1561 TGGTTGGGAATTATCATCAGCTGAGAGAGAGAGAGAGATCTTGTGGTCAACAAAGC 1620  
 DB 1666 TGGTTGGGAATTATCATCAGCTGAGAGAGAGAGAGAGATCTTGTGGTCAACAAAGC 1725  
 QY 1621 AAACCTGAGCTCATCAAGGCTGACATGCTGACGCGCTTCTGTGATTCAGATTC 1680  
 DB 1726 AAACCTGAGCTCATCAAGGCTGACATGCTGACGCGCTTCTGTGATTCAGATTC 1785  
 QY 1681 AGCCACAGGTATCTCCCAACGAGCTTCCGGGGCGAGTCAAGGCCACGCGGGGGGCCA 1740  
 DB 1786 AGCCACAGGTATCTCCCAACGAGCTTCCGGGGCGAGTCAAGGCCACGCGGGGGGCCA 1845  
 QY 1741 GCGGTGTTCCAGAACCGGCTCAAGTTCCAGTTGATATCACTTACACGAGAGGTGGAG 1800  
 DB 1846 GCGGTGTTCCAGAACCGGCTCAAGTTCCAGTTGATATCACTTACACGAGAGGTGGAG 1905  
 QY 1801 GCGCAGAGAGAGAGAGGATCTTACCTCGTCACTTCACTTCACTTCACTTCACTTCA 1860  
 DB 1906 GCGCAGAGAGAGAGAGGATCTTACCTCGTCACTTCACTTCACTTCACTTCACTTCA 1965  
 QY 1861 CGCTTCAAGAGGGTGTGAGAGCAGTCCAGGCGCAGCTGTGAGAGACACAGACCGGCT 1920  
 DB 1966 CGCTTCAAGAGGGTGTGAGAGCAGTCCAGGCGCAGCTGTGAGAGACACAGACCGGCT 2025  
 QY 1921 GCGGCCAGCACTTGTGACAGCAGCTTATCTGATATGAAATGATATGAGGGGCGCTTTC 1980  
 DB 2026 GCGGCCAGCACTTGTGACAGCAGCTTATCTGATATGAAATGATATGAGGGGCGCTTTC 2085  
 QY 1981 AAATGGAATATCCGAAAGTTAA 2007  
 DB 2086 AAATGGAATATCCGAAAGTTAA 2112

RESULT 3  
 US-10-195-071-1





QY	1801	GGCGGAGAAAGSAAACGGGATCTACACCTCCGACCTTCAACCTGCTCTCAAGGCCCCAGCCCGT	1801
Db	1906	GGCGAGAAAGSAAACGGGATCTACACCTCCGACCTTCAACCTGCTCTCAAGGCCCCAGCCCGT	1906
QY	1861	CGCTTCAAGAGGGGTGTGAGACCATCCAGGCCAGCTGTGAGACACACGACCCGCT	1861
Db	1966	CGCTTCAAGAGGGGTGTGAGACCATCCAGGCCAGCTGTGAGACACACGACCCGCT	1966
QY	1921	GGGGCCGACGACTTGTCAACACCACTAACTGTATGAGAAAGATGACGGGGCGGCTTCC	1921
Db	2026	GGGGCCGACGACTTGTCAACACCACTAACTGTATGAGAAAGATGACGGGGCGGCTTCC	2026
QY	1981	AAATGTGAAATTATCCGAAAAGTTAA	2007
Db	2086	AAATGTGAAATTATCCGAAAAGTTAA	2112
RESULT 4			
US-10-195-072-3			
; Sequence 3, Application US/10195072			
; Publication No. US20030092036A1			
; GENERAL INFORMATION:			
; APPLICANT: Origene Technologies			
; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas			
; FILE REFERENCE: 16U 101 C2			
; CURRENT APPLICATION NUMBER: US/10/195, 072			
; CURRENT FILING DATE: 2002-07-15			
; PRIOR APPLICATION NUMBER: US 09/930,181			
; PRIOR FILING DATE: 2001-08-16			
; NUMBER OF SEQ ID NOS: 18			
; SOFTWARE: PatentIn version 3.1.			
; SEQ ID NO: 3			
; LENGTH: 3364			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (482)..(2239)			
; OTHER INFORMATION:			
US-10-195-072-3			
Query Match			
Best Local Similarity 99.3%; Score 1993; DB 15; Length 3364;			
Matches 2007; Conservative 0; Mismatches 0; Indels 4; Gaps 1;			
QY	1	ATGACATGAGCGGGGAGAGACGCGCGCGGACGACGCGGCACTATGTGGGCGCTACCGG	60
Db	229	ATGACATGAGCGGGGAGAGACGCGCGCGGACGACGCGGCACTATGTGGGCGCTACCGG	288
QY	61	CTGGAGAAGCGCTGGGCAAGGGGACAGAGTCTGTGAAGCTGGGGGTTCACTGCCTC	120
Db	289	CTGGAGAAGCGCTGGGCAAGGGGACAGAGTCTGTGAAGCTGGGGGTTCACTGCCTC	348
QY	121	ACCTGCCGAAGGTGGCCATCAAGTGTCAACCGTGAAGAGCTAGCGAGTGGTGTG	180
Db	349	ACCTGCCGAAGGTGGCCATCAAGTGTCAACCGTGAAGAGCTAGCGAGTGGTGTG	408
QY	181	ATGAAGGTGAGCGCGGAGATCGCGATCCTGAAGCTCATTTAGACACCCCGAGTCTTAAG	240
Db	409	ATGAAGGTGAGCGCGGAGATCGCGATCCTGAAGCTCATTTAGACACCCCGAGTCTTAAG	468
QY	241	CTGCACGACGTTTATGAAAACAAAATAATTT---GTACTGGTGTGAAGACGTGTG	296
Db	469	CTGCACGACGTTTATGAAAACAAAATAATTTGTAAGTACTGGTGTGAAGACGTGTG	528
QY	297	AGGTGTAGCTCTTCGACTACCTGTGTGAAGAGGGGAGGCTGACGCTTAAGAGGCTCG	356
Db	529	AGGTGTAGCTCTTCGACTACCTGTGTGAAGAGGGGAGGCTGACGCTTAAGAGGCTCG	588
QY	357	GAACTTCTTCGGCGAGATCATCTTCGCGCTGGAATTTCTGCAACAGCCACTCATATGCGA	416
Db	589	GAACTTCTTCGGCGAGATCATCTTCGCGCTGGAATTTCTGCAACAGCCACTCATATGCGA	648

QY	417	CAGGAGATCTGAAACCTGAAAACCTCTGCTGTGACGAGAAAGAAACAAATCCGACATCGCAGA	476
Db	649	CAGGATCTGAAACCTGAAAACCTCTCTGTGACGAGAAAGAAACAAATCCGATCGCAGA	708
QY	477	CTTTGGACAATGCGGTCCTCGACAGTTTGAGAGAGCTGTGTGAGACACAGCTGTGGTCTCCC	536
Db	709	CTTTGGACATGGGTCCTCGCAGGTTTGGGACAGCCTGTGTGAGACACAGCTGTGGTCTCCC	768
QY	537	CCAATGAGCTTGGCCCTCGAGGTGATTCGGGGGGGAGAAATGATGACGGCCGGAAAGGCGGACGT	596
Db	769	CCAATGAGCTTGGCCCTCGAGGTGATTCGGGGGGGAGAAATGATGACGGCCGGAAAGGCGGACGT	828
QY	597	GTGAGAGCTGCGAGGCTCATCTGTTTCGCTTGTGGTGGGAGGCTCTGACCTTTCGACGATGA	656
Db	829	GTGAGAGCTGCGAGGCTCATCTGTTTCGCTTGTGGTGGGAGGCTCTGACCTTTCGACGATGA	888
QY	657	CAATTCGACAGAGCTGCTGAGAAAGTGAAGCGGGGCGTGTTCACATGCGGCACCTTAT	716
Db	889	CAATTCGACAGAGCTGCTGAGAAAGTGAAGCGGGGCGTGTTCACATGCGGCACCTTAT	948
QY	717	CCCGGCGGACATGCGAGAGTGTGCTAATCGGGGGATATATGAGGTTGAGCGCGGACGCGGCT	776
Db	949	CCCGGCGGACATGCGAGAGTGTGCTAATCGGGGGATATATGAGGTTGAGCGCGGACGCGGCT	1008
QY	777	CACGCTAAGACAAATTCAGAAACAATATGTATATAGGGGGCAAGATGAGCCCGAAC	836
Db	1009	CACGCTAAGACAAATTCAGAAACAATATGTATATAGGGGGCAAGATGAGCCCGAAC	1068
QY	837	AGAGAGAGCCCATTCCTGCGCAAGTGTGCAGATCCGCTCGCTGGCCAGAGCTGTGAGAGCATGGA	896
Db	1069	AGAGAGAGCCCATTCCTGCGCAAGTGTGCAGATCCGCTCGCTGGCCAGAGCTGTGAGAGCATGGA	1128
QY	897	CCCGGACGCTGCTGTGACAGCATGCACTCACTGAGCTGCTTCCGAGACCGCAACAGCTGCT	956
Db	1129	CCCGGAGGCTGTGAGACAGCATGCACTCACTGAGCTGCTTCCGAGACCGCAACAGCTGCT	1188
QY	957	GCAGGACCTGCTGTTCGAGAGAGAGAACCAAGAGAAATGATTTACTTCTCTCTCTGGA	1016
Db	1189	GCAGGACCTGCTGTTCGAGAGAGAGAACCAAGAGAAATGATTTACTTCTCTCTCTGGA	1248
QY	1017	CCGGAAGAAAGATACCCGAGCCGAGAGAGATGAGGACCTGCCCCCGGAAAGAGATGGA	1076
Db	1249	CCGGAAGAAAGATACCCGAGCCGAGAGAGATGAGGACCTGCCCCCGGAAAGAGATGGA	1308
QY	1077	CCCTTCCCGAAGCGTGTGAATCCCGAGTGTGAACCGGACCGGCAAGCGGCGGCGACA	1136
Db	1309	CCCTTCCCGAAGCGTGTGAATCCCGAGTGTGAACCGGACCGGCAAGCGGCGGCGACA	1368
QY	1137	AAGCAAAATCCATGAGAGGTGCTCAAGGTGACGAGAGGAGGAGGAGGCTCCCGGAGCTGGGCGGAG	1196
Db	1369	AAGCAAAATCCATGAGAGGTGCTCAAGGTGACGAGAGGAGGAGGAGGCTCCCGGAGCTGGGCGGAG	1428
QY	1197	GAGCAATGAGATGGCCCGACGACGAGGAGCTTCGTGCATCAAGCGGTGTCTCTCTCAGG	1256
Db	1429	GAGCAATGAGATGGCCCGACGACGAGGAGCTTCGTGCATCAAGCGGTGTCTCTCTCAGG	1488
QY	1257	CCTTTTCCACGAGCCCACTCAAGAGCCCTCCGGGTGAACCTCTTACACCTCTTACCAAGGAGAG	1316
Db	1489	CCTTTTCCACGAGCCCACTCAAGAGCCCTCCGGGTGAACCTCTTACACCTCTTACCAAGGAGAG	1548
QY	1317	TCCCTTCCCAAGCCCGCAAGGAGGAGACCTGTTCACAGCGCAAAAGAGAGACCGGCTGGAC	1376
Db	1549	TCCCTTCCCAAGCCCGCAAGGAGGAGACCTGTTCACAGCGCAAAAGAGAGACCGGCTGGAC	1608
QY	1377	GCCCAATCCCAAGGCTCCCTGTCAAGCTCCAGGCTTGAAGGGGTGCCCTTGAAGGGCGGAGCT	1436
Db	1609	GCCCAATCCCAAGGCTCCCTGTCAAGCTCCAGGCTTGAAGGGGTGCCCTTGAAGGGCGGAGCT	1668
QY	1437	CAACTCCATCAAGAAACAGCTTTCTGTGGGTCAACCCGCTTTCACAGCGCGGGAACATGTCAAGT	1496
Db	1669	CAACTCCATCAAGAAACAGCTTTCTGTGGGTCAACCCGCTTTCACAGCGCGGGAACATGTCAAGT	1728
QY	1497	TCCGACGCGGAGGAGATGTCCAACTGACACAGAGTGTCTCCCGAGAGCTTGGCGAAGAA	1556





QY 582 CCGAAGGCGAGAGTGTGAGCTGCGGCTGATCTGTTGCGCTTGCGTGGGCGCTCT 641  
Db 570 CCGGAAGCGGAGAGTGTGAGCTGCGGCGTCACTGTTGCTTGCTGCTGGGCGCTCT 629  
QY 642 GCGCTTGAAGATGACATTTGGGACAGCTGCTGGAGAGATTAACCGGCGCTGTTTCA 701  
Db 630 GCGCTTGAAGATGACATTTGGGACAGCTGCTGGAGAGATTAACCGGCGCTGTTTCA 689  
QY 702 CATGCGGACATTTATCCCGCCGCACTGCGAGATGCTGCTGAGGCGGATGATCGAGTGA 761  
Db 690 CATGCGGACATTTATCCCGCCGCACTGCGAGATGCTGCTGAGGCGGATGATCGAGTGA 749  
QY 762 GCGCGACGCGCGCTGACGCTGAGACATTTCAAGAAACATATGTTATATAGGGGCA 821  
Db 750 GCGCGACGCGCGCTGACGCTGAGACATTTCAAGAAACATATGTTATATAGGGGCA 809  
QY 822 GAATGAGCGCGAGACAGAGAGCGCATTTCTCGAAGGTGACAGATCGCTGCGCGCA 881  
Db 810 GAATGAGCGCGAGACAGAGAGCGCATTTCTCGAAGGTGACAGATCGCTGCGCGCA 869  
QY 882 CTTGAGAGACATCGAGCGCGAGCGTGTGACAGATGACATCTGCGGCTGCTTCCGAGA 941  
Db 870 CTTGAGAGACATCGAGCGCGAGCGTGTGACAGATGACATCTGCGGCTGCTTCCGAGA 929  
QY 942 CCGGAAGAGCTGTGAGAGACCTGCTGCGAGAGAGAGACAGAGAGATGATTA 1001  
Db 930 CCGGAAGAGCTGTGAGAGACCTGCTGCGAGAGAGAGACAGAGAGATGATTA 989  
QY 1002 CTTCTCTCTCTGTGAGCGGAAAGAAAGATACCGAGCGAGAGATGAGACCTGCGCCC 1061  
Db 990 CTTCTCTCTCTGTGAGCGGAAAGAAAGATACCGAGCGAGAGATGAGACCTGCGCCC 1049  
QY 1062 CCGGAAGAGATTAACCTTCCCGGAGCGGTGAGATCTCCCGATGCTGAACCGGAGCG 1121  
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QY 1122 CAAGCGCGCGGACAGAGCAATTCATGAGGTGCTGAGGTGACGAGCGGCGCTCCCC 1181  
Db 1110 CAAGCGCGCGGACAGAGCAATTCATGAGGTGCTGAGGTGACGAGCGGCGCTCCCC 1169  
QY 1182 GGTGCTGTGCGGCGGCGGATGAGATGAGCGGACAGCGGCAAGGTCTTGCTCATGAG 1241  
Db 1170 GGTGCTGTGCGGCGGCGGATGAGATGAGCGGACAGCGGCAAGGTCTTGCTCATGAG 1229  
QY 1242 CCGTGTGCTCTGAGGCTTTTCCACAGCGGCACTGAGAGCGGCGGCTGACCGCTGACCC 1301  
Db 1230 CCGTGTGCTCTGAGGCTTTTCCACAGCGGCACTGAGAGCGGCGGCTGACCGCTGACCC 1289  
QY 1302 CTCACCAAGGGGAGTCCCTTCCACAGCGGCACTGAGAGCGGCGGCTGACCGCTGACCC 1361  
Db 1290 CTCACCAAGGGGAGTCCCTTCCACAGCGGCACTGAGAGCGGCGGCTGACCGCTGACCC 1349  
QY 1362 GAGCGCGGCTGAGCGGCGGCACTGAGAGCGGCGGCTGAGAGCGGCGGCTGAGCGG 1421  
Db 1350 GAGCGCGGCTGAGCGGCGGCACTGAGAGCGGCGGCTGAGAGCGGCGGCTGAGCGG 1409  
QY 1422 CTGAGAGCGGCGGCTGAGAGCGGCTTCTGAGGCTGACCGGCTTCCACCG 1481  
Db 1410 CTGAGAGCGGCGGCTGAGAGCGGCTTCTGAGGCTGACCGGCTTCCACCG 1469  
QY 1482 CCGGAAATGCAAGTTCTGAGAGCGGCGGAGATTTCCAACTGACACCAAGAGTGTCC 1541  
Db 1470 CCGGAAATGCAAGTTCTGAGAGCGGCGGAGATTTCCAACTGACACCAAGAGTGTCC 1529  
QY 1542 AGAGCTGAGAGAGAGTCTGTTGGAACTTTCATGAGCTGAGAGAGAGAGAGAGAT 1601  
Db 1530 AGAGCTGAGAGAGAGTCTGTTGGAACTTTCATGAGCTGAGAGAGAGAGAGAT 1589  
QY 1602 CTTGTGTGATCAAAAGCAAACTCTGAGCTTCATGAGGCTGACATCTGTGACGCTT 1661  
Db 1590 CTTGTGTGATCAAAAGCAAACTCTGAGCTTCATGAGGCTGACATCTGTGACGCTT 1649

QY 1662 CTTGTGATTTCCAGTCTACAGCCACAGGCTGATCTCCCAAGAGAGCTTCCGGGCGAGTA 1721  
Db 1650 CTTGTGATTTCCAGTCTACAGCCACAGGCTGATCTCCCAAGAGAGCTTCCGGGCGAGTA 1709  
QY 1722 CAAGGCGACGCGGCGGCGAGCGGCTGTTCCAGAGCGGCTCAAGTTCCAGGTTGATATAC 1781  
Db 1710 CAAGGCGACGCGGCGGCGAGCGGCTGTTCCAGAGCGGCTCAAGTTCCAGGTTGATATAC 1769  
QY 1782 CTACACGAGGAGTGGGAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1841  
Db 1770 CTACACGAGGAGTGGGAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1829  
QY 1842 GCTCTCAGGCGGCGGCGGCTTCCAGAGGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAG 1901  
Db 1830 GCTCTCAGGCGGCGGCGGCTTCCAGAGGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAG 1889  
QY 1902 GAGCACACAGACCGGCTGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1961  
Db 1890 GAGCACACAGACCGGCTGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1949  
QY 1962 GATGACGCGGCGGCTTCCAAATGAGATTAATCCGAAAGATTAA 2007  
Db 1950 GATGACGCGGCGGCTTCCAAATGAGATTAATCCGAAAGATTAA 1995

RESULT 7  
US-10-288-798-42  
Sequence 42, Application US/10288798  
Publication No. US20030207299A1  
GENERAL INFORMATION:  
APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B.;  
APPLICANT: WALIA, Nardinder K.; HARFALIA, April J.A.;  
APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;  
APPLICANT: GURURAJAN, Rajagopal; DING, Li;  
APPLICANT: PATTERSON, Chandra; YUE, Henry;  
APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;  
APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;  
APPLICANT: LU, Yan; ISON, Craig H.; Y. Tom;  
APPLICANT: AU-YOUNG, Janice; TANG, Y. Tom;  
APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;  
APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;  
APPLICANT: LU, Dnyang Aina M.; LAU, Preeti G.;  
APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;  
APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;  
APPLICANT: THANGAVELOU, Kavitha; BURFORD, Neil  
TITLE OF INVENTION: HUMAN KINASES  
FILE REFERENCE: PI-0209 USA  
CURRENT APPLICATION NUMBER: US/10/288,798  
CURRENT FILING DATE: 2002-11-01  
PRIOR APPLICATION NUMBER: PCT/US01/27219  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/240,542  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/238,389  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 60/236,499  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: US 60/234,902  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: US 60/232,654  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: US 60/231,357  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: US 60/229,873  
PRIOR FILING DATE: 2000-08-31  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PERL Program  
SEQ ID NO: 42  
LENGTH: 2647  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature

OTHER INFORMATION: Incyte ID No. US20030207299A1 4022651CB1  
 US-10-288-798-42

Query Match 98.0%; Score 1966; DB 16; Length 2647;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1966; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 42 GTATGTTGGGCGCTTACCGGCTGAGAGAGACCTGGGCAAGGGGCAAGCTGTGTGA 101
D 30 GTATGTTGGGCGCTTACCGGCTGAGAGAGACCTGGGCAAGGGGCAAGCTGTGTGA 89
QY 102 GCTGGGGGTTCACTGCTCACTCCCGAGAGGTGGCCATCAAGTCTGTCAACCTGTGA 161
D 90 GCTGGGGGTTCACTGCTCACTCCCGAGAGGTGGCCATCAAGTCTGTCAACCTGTGA 149
QY 162 GCTCAGAGAGTGGGTGTGATGAAGAGTGAAGCGGAGATCGCATCTGTAGGCTCATTTGA 221
D 150 GCTCAGAGAGTGGGTGTGATGAAGAGTGAAGCGGAGATCGCATCTGTAGGCTCATTTGA 209
QY 222 GCACCCCGACGTCTTAAGCTGACGAGCTTTATGAAAACAAAATATTTGTAACCTGT 281
D 210 GCACCCCGACGTCTTAAGCTGACGAGCTTTATGAAAACAAAATATTTGTAACCTGT 269
QY 282 GCTAGAACAGGTGTGAGTGTGAGTCTTTCGACTACCTGTGTGAAGAGAGGAGCTGAC 341
D 270 GCTAGAACAGGTGTGAGTGTGAGTCTTTCGACTACCTGTGTGAAGAGAGGAGCTGAC 329
QY 342 GCCTAAGAGAGCTCGAAGTCTTCCGAGATCATCTGCGCTGTGACTTTCGCAAG 401
D 330 GCCTAAGAGAGCTCGAAGTCTTCCGAGATCATCTGCGCTGTGACTTTCGCAAG 389
QY 402 CCATCTCATATGCGACAGGATCTGAAACCTGAAACCTCTCTGTGAAGAGAGAGCA 461
D 390 CCATCTCATATGCGACAGGATCTGAAACCTGAAACCTCTCTGTGAAGAGAGAGCA 449
QY 462 CATCCGATCGACAGCTTTGGAGTGGTCCCTGCAAGTGTGAGAGAGCTGTGTGAGAG 521
D 450 CATCCGATCGACAGCTTTGGAGTGGTCCCTGCAAGTGTGAGAGAGCTGTGTGAGAG 509
QY 522 CAGCTGTGGGTCCCCCACTACGCTTCCGAGAGTGTATCCGGGGGAGAGATGAAG 581
D 510 CAGCTGTGGGTCCCCCACTACGCTTCCGAGAGTGTATCCGGGGGAGAGATGAAG 569
QY 582 CCGGAGAGCGGAGCTGTGAGCTGCGGCGTCACTCTTGCGCTGTGTGTGGGGGCT 641
D 570 CCGGAGAGCGGAGCTGTGAGCTGCGGCGTCACTCTTGCGCTGTGTGTGGGGGCT 629
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D 630 GCCCTTCGAGATGACAACTTTCGACAGCTGTGTGAGAGAGTGAAGCGGGGCTGTTC 689
QY 702 CATCCCGCACTTTATCCCGCCCGCATGCGAGAGTGTCTAAGGGGCAATGATGAGTGA 761
D 690 CATCCCGCACTTTATCCCGCCCGCATGCGAGAGTGTCTAAGGGGCAATGATGAGTGA 749
QY 762 CGCGGCAAGCGGCTCTGAGTGAAGCATTTCAAGAAACATATGTATATAGGGGCA 821
D 750 CGCGGCAAGCGGCTCTGAGTGAAGCATTTCAAGAAACATATGTATATAGGGGCA 809
QY 822 GAATGAGCTCGGAAACCAAGAGAGCCATTCTTCCGAAGTGAAGTCCGCTGCTGCCAG 881
D 810 GAATGAGCTCGGAAACCAAGAGAGCCATTCTTCCGAAGTGAAGTCCGCTGCTGCCAG 869
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D 870 CCTGAGAGAGCATGACCCCGAGCTGTGAGACAGCATCACTACTGGGCTGTTCGAG 929
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D 930 CCGGAAAGAGTGTGAGAGAGCTGTGTGAGAGAGAGAGAGAGAGAGATGATTA 989
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D 1110 CAGGCGGCGGCAAGACGCAATTCATGAGTGTCTCAGCTGTGAGAGAGCTGTGCC 1169
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D 1470 CCGGAAAGTGAAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1529
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RESULT 8  
 US-10-283-247-1  
 ; Sequence 1, Application US/10283247  
 ; Publication No. US20030119037A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NEBLAM, Beena et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
FILE REFERENCE: CL001304  
CURRENT APPLICATION NUMBER: US/10/283,247  
CURRENT FILING DATE: 2002-10-30  
NUMBER OF SEQ. ID NOS: 10  
SOFTWARE: PASTSEQ for Windows Version 4.0  
SEQ ID NO: 1  
LENGTH: 2025  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-283-247-1

Query Match 96.7%; Score 1941.2; DB 15; Length 2025;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1943; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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481 GGCATGGGCTCTCTGCGAGTGTGGCAGACGCTTGTGAGACCAAGCTGTGGTCCCCCAG 540  
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601 AGCTGGCGGCTCATCTGTTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 660  
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QY 1921 GCGGCCAGCACTTGTGAGACACAC 1946  
DB 1921 GCGGCCAGCACTTGTGAGAACCCCC 1946

## RESULT 9

US-09-842-582-3  
; Sequence 3, Application US/09842582  
; Patent No. US20020155570A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Meyers, Rachel  
; TITLE OF INVENTION: 2246, NOVEL PROTEIN KINASE MOLECULES AND  
; FILE REFERENCE: 38155-20054.00  
; CURRENT APPLICATION NUMBER: US/09/842,582  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2025  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-842-582-3

Query Match 96.6%; Score 1939.6; DB 9; Length 2025;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 194; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGACATCGACGGGAGAGACGGCGCGCAGCAGCGCATGATGTTGGGCCCCCTAACCG 60  
DB 1 ATGACATCGACGGGAGAGAGACGGCGCGCAGCAGCGCATGATGTTGGGCCCCCTAACCG 60  
QY 61 CTGGAAGAGAGCGCTGGGCGAAGGGGCGAGACAGGTCTGGTGAAGCTGGGGGGTCTACTGCGTC 120  
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DB 121 ACCCTGCAGAGAGTGGCCATCAAGATCGTCAACCGTGAAGCTCAGCGAGTGGTCTG 180  
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DB 301 GGTGAGCTCTTCCACTACCTGCTGAGAGAGAGGAGGCTTAAAGAGGCTCGAAG 360  
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Db 1921 GCGGCCAGACCTTGTGACAGACCCAC 1946

RESULT 10  
US-09-842-582-1  
Sequence 1, Application US/09842582  
Patent No. US20020155570A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Meyers, Rachel  
TITLE OF INVENTION: 2246, NOVEL PROTEIN KINASE MOLECULES AND  
TITLE OF INVENTION: US85 THEREFOR  
FILE REFERENCE: 38155-20054.00  
CURRENT APPLICATION NUMBER: US/09/842,582  
PRIORITY FILING DATE: 2001-04-25  
PRIORITY APPLICATION NUMBER: US 60/199,391  
PRIORITY FILING DATE: 2000-04-25  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2219  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (53)....(2077)  
US-09-842-582-1

Query Match 96.6%; Score 1939.6; DB 9; Length 2219;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1942; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGACATCGACGGGAGAAAGACGGCGCGCGACAGCAGCATGATGTTGGCCCTTACCGG 60  
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QY 1501 ACGCCGAGAGATGTCTCAACTGACACAGAGTCTGCCAGAGTGGCGGAAGATCC 1560
DB 1553 ACGCCGAGAGATGTCTCAACTGACACAGAGTCTGCCAGAGTGGCGGAAGATCC 1612
QY 1561 TGGTTGGGAACTTCATCAGGCTGGAGAGAGAGAGATCTTCGTGCATCAAGAC 1620
DB 1613 TGGTTGGGAACTTCATCAGGCTGGAGAGAGAGAGATCTTCGTGCATCAAGAC 1672
QY 1621 AAACCTTGAGCTTCATCAAGAGCTGACATGTGCAGCCCTTCCTGTCAATTCGAGTCTC 1680
DB 1673 AAACCTTGAGCTTCATCAAGAGCTGACATGTGCAGCCCTTCCTGTCAATTCGAGTCTC 1732
QY 1681 AGCCACAGCTCATCTCCCAAGAGAGCTCCGAGCGAGTACAAAGGCCAGGGGGGGCCA 1740
DB 1733 AGCCACAGCTCATCTCCCAAGAGAGCTCCGAGCGAGTACAAAGGCCAGGGGGGGCCA 1792
QY 1741 GCCGTGTTCCAGAAAGCCGATCAAGTTCCAGTTGATATCACTACAGAGAGGTGGAGAG 1800
DB 1793 GCCGTGTTCCAGAAAGCCGATCAAGTTCCAGTTGATATCACTACAGAGAGGTGGAGAG 1852
QY 1801 GCGGAGAGAGAGAGAGAGAGATCTACCTGTCACCTTCACCTGCTTCAGAGCCCGACGCT 1860
DB 1853 GCGGAGAGAGAGAGAGAGATCTACCTGTCACCTTCACCTGCTTCAGAGCCCGACGCT 1912
QY 1861 CGCTTCAAGAGAGGTGTGAGAGACCATCCAGGCCAGCTGTGAGACACACAGCCGCT 1920
DB 1913 CGCTTCAAGAGAGGTGTGAGAGACCATCCAGGCCAGCTGTGAGACACACAGCCGCT 1972
QY 1921 GCGGCCCGACCATCTGTGTACAGACCAAC 1946
DB 1973 GCGGCCCGACCATCTGTGTACAGACCAAC 1998

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RESULT 11
US-10-054-579-3
; Sequence 3, Application US/10054579
; Publication No. US20020137913A1
; GENERAL INFORMATION:
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. US20020137913A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0300-USA
; CURRENT APPLICATION NUMBER: US/10/054,579
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,378
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-579-3

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Query Match 31.0%; Score 1827; DB 14; Length 1827;
Seq. Local Similarity 100.0%; Pred. No. 0;
Matches 1827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 ATGAAGTGAAGAGAGAGATGCGATCCTGAAGCTCATTTGAGCAACCCCAAGCTCTTAAG 240
DB 1 ATGAAGTGAAGAGAGAGATGCGATCCTGAAGCTCATTTGAGCAACCCCAAGCTCTTAAG 60
QY 241 CTGACAGACGTTTATGAAAAAATAATTTTGAAGCTGTGCTGTAAGAACGTCTCAGT 300
DB 61 CTGACAGACGTTTATGAAAAAATAATTTTGAAGCTGTGCTGTAAGAACGTCTCAGT 120
QY 301 GGTAGAGCTCTGACACTGCTGTGAAGAGAGAGAGCTGACGCTTAAGAGAGCTCGAGAG 360
DB 121 GGTAGAGCTCTGACACTGCTGTGAAGAGAGAGAGCTGACGCTTAAGAGAGCTCGAGAG 180
QY 361 TTCTTCCGAGATCATCTGTGCGCTGAGCTTCTGCAACAGCACTCCATATGCGCAGG 420

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DB 181 TTCTTCCGAGATCATCTGTGCGCTGAGACTTCTGCAACAGCACTCCATATGCGCAGG 240
QY 421 GATCTGAACCTTGAAAACTCTGCTGAGACGAGAGAAACAACTTCGATGCGACATTT 480
DB 241 GATCTGAACCTTGAAAACTCTGCTGAGACGAGAGAAACAACTTCGATGCGACATTT 300
QY 481 GGTATGAGCTCTGCTGAGAGTGGAGACAGCTGTTGAGAGACAGCTGTGAGTCCCCCAG 540
DB 301 GGTATGAGCTCTGCTGAGAGTGGAGACAGCTGTTGAGAGACAGCTGTGAGTCCCCCAG 360
QY 541 TACGCTGCGCGAGAGTGAATCCGAGGAGAGAAATATGACGCGCGAGAGCGTGTG 600
DB 361 TACGCTGCGCGAGAGTGAATCCGAGGAGAGAAATATGACGCGCGAGAGCGTGTG 420
QY 601 AGCTGCGAGCTCATCTGTTGCGCTTGTGCTGAGTGGAGAGTCTGCGCTTGAAGATGAC 660
DB 421 AGCTGCGAGCTCATCTGTTGCGCTTGTGCTGAGTGGAGAGTCTGCGCTTGAAGATGAC 480
QY 661 TTGCGACAGCTCTGAGAGAGTGAAGCGAGGCGTGTTCACATGCGGACCTTATCCG 720
DB 481 TTGCGACAGCTCTGAGAGAGTGAAGCGAGGCGTGTTCACATGCGGACCTTATCCG 540
QY 721 CCGGACTGCGACAGTCTGTACGAGGACATGATCGAGTGAAGCGCGACGCGCTCAG 780
DB 541 CCGGACTGCGACAGTCTGTACGAGGACATGATCGAGTGAAGCGCGACGCGCTCAG 600
QY 781 CTAGAGACATTCAGAAACATATGATATAGAGGAGAGAGATGAGCCGACAGAG 840
DB 601 CTAGAGACATTCAGAAACATATGATATAGAGGAGAGAGATGAGCCGACAGAG 660
QY 841 CAGCCCATCTCTGCAAGGTGCAATCCGCTGCTGCGCACGCTGAGAGACATGACCCC 900
DB 661 CAGCCCATCTCTGCAAGGTGCAATCCGCTGCTGCGCACGCTGAGAGACATGACCCC 720
QY 901 GAGTGTGAGAGAGATGACATCACTGAGGCTGCTCCGAGACCGGACAGCTGTGAG 960
DB 721 GAGTGTGAGAGAGATGACATCACTGAGGCTGCTCCGAGACCGGACAGCTGTGAG 780
QY 961 GACTGCTGTCCGAGAGAGAGACCAAGAGATGATTACTTCTCTCTGAGCCG 1020
DB 781 GACTGCTGTCCGAGAGAGAGACCAAGAGATGATTACTTCTCTCTGAGCCG 840
QY 1021 AAGAGAGGTATCCGAGAGAGAGATGAGACCTGCCCCCGGAGAGAGATGAGT 1080
DB 841 AAGAGAGGTATCCGAGAGAGAGATGAGACCTGCCCCCGGAGAGAGATGAGT 900
QY 1081 CCGCGAGAGCTGTGAGATCCCGATGCTGAACCGGACAGGACGCGGCGCAGAACGC 1140
DB 901 CCGCGAGAGCTGTGAGATCCCGATGCTGAACCGGACAGGACGCGGCGCAGAACGC 960
QY 1141 AATTCATGAGAGTGTGAGAGCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 961 AATTCATGAGAGTGTGAGAGCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1201 ATTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1021 ATTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1261 TCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1081 TCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1321 CTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1141 CTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1381 AACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1201 AACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1441 TCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1261 TCCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320

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QY 1501 ACGCCGAGAGGATGTCACCTTGACACAGAGTGTCCCGCAGAGCTGCGGAGAGATGCC 1560  
 DB 1321 ACGCCGAGAGGATGTCACCTTGACACAGAGTGTCCCGCAGAGCTGCGGAGAGATGCC 1380  
 QY 1561 TGGTTTGGGAACTTCATCAGCTTGAGAGAGAGAGAGATCTTCTGTGTCATCAAAAGAC 1620  
 DB 1381 TGGTTTGGGAACTTCATCAGCTTGAGAGAGAGAGAGATCTTCTGTGTCATCAAAAGAC 1440  
 QY 1621 AAACCTGTAGCTTCATCAAGGCTGAGATGTCAGGCTTCCTGTGTGATTCAGAGCTTC 1680  
 DB 1441 AAACCTGTAGCTTCATCAAGGCTGAGATGTCAGGCTTCCTGTGTGATTCAGAGCTTC 1500  
 QY 1681 AGCCACAGGCTCATCTCCCAAACGAGCTTCGCGGCCGAGTCAAGAGCCAGCGGGGGCCCA 1740  
 DB 1501 AGCCACAGGCTCATCTCCCAAACGAGCTTCGCGGCCGAGTCAAGAGCCAGCGGGGGCCCA 1560  
 QY 1741 GCCGTGTCCAGAAAGCCGCTCAAGTTCAGAGTGTATCTACCTACACCGAGGGGTGGGGAG 1800  
 DB 1561 GCCGTGTCCAGAAAGCCGCTCAAGTTCAGAGTGTATCTACCTACACCGAGGGGTGGGGAG 1620  
 QY 1801 GCGGAGAGAGAGAGAGGAGCTTACCTCCGTCACCTTCAGGCTTCAGGCTCCAGGCTTC 1860  
 DB 1621 GCGGAGAGAGAGAGAGGAGCTTACCTCCGTCACCTTCAGGCTTCAGGCTCCAGGCTTC 1680  
 QY 1861 CGCTTCAAGAGGCTGTGTGAGAGACCATCAAGGCCCAAGCTGCTGAGACACACGAGCCCT 1920  
 DB 1681 CGCTTCAAGAGGCTGTGTGAGAGACCATCAAGGCCCAAGCTGCTGAGACACACGAGCCCT 1740  
 QY 1921 GCGGCCCAAGGCTGTGTGAGAGACCATCAAGTGTGAGAAATGATGACGCGGGGCTTTCC 1980  
 DB 1741 GCGGCCCAAGGCTGTGTGAGAGACCATCAAGTGTGAGAAATGATGACGCGGGGCTTTCC 1800  
 QY 1981 AATGTGGAATTAATCCGAAAGTTAA 2007  
 DB 1801 AATGTGGAATTAATCCGAAAGTTAA 1827

RESULT 12  
 US-10-425-114-26842  
 ; Sequence 26842, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhu, Jindong  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E  
 ; APPLICANT: Tabaska, Jack E  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(5313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; NUMBER OF SEQ ID NOS: 2003-04-28  
 ; SEQ ID NO 26842  
 ; LENGTH: 3791  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB4651-024-E4\_FLI  
 US-10-425-114-26842

Query Match 88.6%; Score 1777.4; DB 13; Length 3791;  
 Best Local Similarity 96.3%; Pred. No. 0;  
 Matches 1857; Conservative 0; Mismatches 6; Indels 66; Gaps 1;  
 QY 84 GCGAGCAGGCTGTGTGAGAGTGGGGGTTCACTGCTCACTTCCAGAGAGTGGGATCAA 143  
 DB 62 GCGTCAAGGCTGTGTGAGAGTGGGGGTTCACTGCTCACTTCCAGAGAGTGGGATCAA 121  
 QY 144 GATGTCAACGCTGAGAGCTCAAGGAGTGGGTGTGTAAGGTGAGCGGAGATCGC 203

DB 122 GATGTCAACGCTGAGAGCTCAAGGAGTGGGTGTGTAAGGTGAGCGGAGATCGC 181  
 QY 204 GATCTGAAGCTCAATTGAGCACCCCACTGCTCAAGCTGACAGACCTTTATGAAAA 263  
 DB 182 GATCTGAAGCTCAATTGAGCACCCCACTGCTCAAGCTGACAGACCTTTATGAAAA 241  
 QY 264 AAAATATTGTGACCTGTGTGTAAGACAGTGTCAAGTGTGAGAGTCTTCCAGCTGCT 323  
 DB 242 AAAATATTGTGACCTGTGTGTAAGACAGTGTCAAGTGTGAGAGTCTTCCAGCTGCT 301  
 QY 324 GAAAGAGGGAGGCTGACGCTTAAGAGAGGCTGGAAGTCTTCCGAGAGATCATCTGTC 383  
 DB 302 GAAAGAGGGAGGCTGACGCTTAAGAGAGGCTGGAAGTCTTCCGAGAGATCATCTGTC 361  
 QY 384 GCTGACCTTCTGCAACAGCTCTCATATGCAACAGGATTTGAAACCTGAAAACTCTCT 443  
 DB 362 GCTGACCTTCTGCAACAGCTCTCATATGCAACAGGATTTGAAACCTGAAAACTCTCT 421  
 QY 444 GCTGACGAGAGAAACAATCCGATGACAGCTTTGACATGAGCTTCCTGACAGTTGG 503  
 DB 422 GCTGACGAGAGAAACAATCCGATGACAGCTTTGACATGAGCTTCCTGACAGTTGG 481  
 QY 504 CGACAGCTGTTGAGACCAAGCTGTGCTCCCACTACGCTGCTCCGAGGTGATCCG 563  
 DB 482 CGACAGCTGTTGAGACCAAGCTGTGCTCCCACTACGCTGCTCCGAGGTGATCCG 541  
 QY 564 GGGGAGAGATGATGACGCGCCGAGAGGAGGAGAGTGTGAGAGTGTGAGAGTGTGAG 623  
 DB 542 GGGGAGAGATGATGACGCGCCGAGAGGAGGAGAGTGTGAGAGTGTGAGAGTGTGAG 601  
 QY 624 CTTCGTGTGAGGAGCTGTGCTGCTTGAAGATGACAACTTGTGAGAGTGTGAGAGT 683  
 DB 602 CTTCGTGTGAGGAGCTGTGCTGCTTGAAGATGACAACTTGTGAGAGTGTGAGAGT 661  
 QY 684 GAAAGGAGGAGCTGTGCTGCAATGCGCACTTTATCCCGCGAGCTGCAAGTGTGAG 743  
 DB 662 GAAAGGAGGAGCTGTGCTGCAATGCGCACTTTATCCCGCGAGCTGCAAGTGTGAG 721  
 QY 744 GGGCATGATGAGAGTGAAGCGCGGACCGGCTCAAGCTGAGAGCAATTCAGAAACAT 803  
 DB 722 GGGCATGATGAGAGTGAAGCGCGGACCGGCTCAAGCTGAGAGCAATTCAGAAACAT 781  
 QY 804 ATGTATATAGGGGGGAGAGATGAGCCCGAACCAGAGAGCCATTTCTTCCAGAGTGA 863  
 DB 782 ATGTATATAGGGGGGAGAGATGAGCCCGAACCAGAGAGCCATTTCTTCCAGAGTGA 841  
 QY 864 GATCCGCTGCTGCGCCAGCTGAGAGCATGACCCCGAGCTGTGACAGATGACTTC 923  
 DB 842 GATCCGCTGCTGCGCCAGCTGAGAGCATGACCCCGAGCTGTGACAGATGACTTC 901  
 QY 924 ACTGAGCTGCTTCCGAGACCGGACAGCAAGCTGTGAGAGCTGCTGTCCGAGAGAGAA 983  
 DB 902 ACTGAGCTGCTTCCGAGACCGGACAGCAAGCTGTGAGAGCTGCTGTCCGAGAGAGAA 961  
 QY 984 CCAGAGAGAGATGATTTACTTCTCTCTGAGACCGGAAAGAGTACCAGGACAGGA 1043  
 DB 962 CCAGAGAGAGATGATTTACTTCTCTCTGAGACCGGAAAGAGTACCAGGACAGGA 1021  
 QY 1044 GGATGAGAGCTGCCCCCGGAGAGAGATGACCTTCCCGGAGGCTGTGACTCC 1103  
 DB 1022 GGATGAGAGCTGCCCCCGGAGAGAGATGACCTTCCCGGAGGCTGTGACTCC 1081  
 QY 1104 GATGCTGAACCGGACCGGACAGGCGGCGGAGAGAGATTCATGAGAGTGTGAGAGT 1163  
 DB 1082 GATGCTGAACCGGACCGGACAGGCGGCGGAGAGAGATTCATGAGAGTGTGAGAGT 1141  
 QY 1164 GACGACGCGGCTCCCGGCTGCTGCGCGGCGGCTTGAAGTGTGAGAGCGGCA 1223  
 DB 1142 GACGACGCGGCTCCCGGCTGCTGCGCGGCGGCTTGAAGTGTGAGAGCGGCA 1201  
 QY 1224 G----- 1224  
 DB 1202 GAGTAAGCAATGTTCAATAAAGCTGTGATATGCTGAGGCCATCCCAATTACAGA 1261

QY	1225	-----AGGCTGGGTGCATCAGCGGCGCTCTCTAGGCGCTTTCACACAGCCACTCAG	1277
Db	1262	AGAAAGACAGGCTCTCGGTTCATCAGCGGTGCTCTCTCAGGCGCTTTCACACAGCCACTCAG	1321
QY	1278	CAGCCCCCGGGTGAACCCCTCACCCTCACCAGGAGGAGTCCCTCCCAACCCCGCAAGG	1337
Db	1322	CAGCCCCCGGGTGAACCCCTCACCCTCACCAGGAGGAGTCCCTCCCAACCCCGCAAGG	1381
QY	1338	GACACCTGTCCACACGCGCAAAAGAGAGCCCGGCTGGCAGCGCCCAACCCCAAGCCCCGTC	1397
Db	1382	GACACCTGTCCACACGCGCAAAAGAGAGCCCGGCTGGCAGCGCCCAACCCCAAGCCCCGTC	1441
QY	1398	CAGCCCCCAGGTGGAGAGGGGTTGCCCTGGAGGGCGCGGCTCACTCCATCAAGAACACTT	1457
Db	1442	CAGCCCCCAGGTGGAGAGGGGTTGCCCTGGAGGGCGCGGCTCACTCCATCAAGAACACTT	1501
QY	1458	TCTGGGCTCACCCTCGCTTCCACGCGCCGGAACCTGCAAGTTCCGACGCGCGAGAGATGTC	1517
Db	1502	TCTGGGCTCACCCTCGCTTCCACGCGCCGGAACCTGCAAGTTCCGACGCGCGAGAGATGTC	1561
QY	1518	CACCTTGACACCAAGAGTGTCTCCCAAGAGCTGGCCAAAGATCTCGTTTGGGAATTCTAT	1577
Db	1562	CACCTTGACACCAAGAGTGTCTCCCAAGAGCTGGCCAAAGATCTCGTTTGGGAATTCTAT	1621
QY	1578	CAGCTGGAGAAAGAGAGAGAGATCTTGCTGATCATCAAGACAAACCTCTGAGCTCAT	1637
Db	1622	CAGCTGGAGAAAGAGAGAGAGATCTTGCTGATCATCAAGACAAACCTCTGAGCTCAT	1681
QY	1638	CAGGCTGACATCTGTCAAGCGCTTCTGTGATTCAGATCTCAGGCCACAGCGTCATCTC	1697
Db	1682	CAGGCTGACATCTGTGCAAGCGCTTCTGTGATTCAGATCTCAGGCCACAGCGTCATCTC	1741
QY	1698	CCAAACGAGCTTCCGGGCGGAGTACAAAGCCACCGGGGGGCGACCGGTTCCAGAAAGCC	1757
Db	1742	CCAAACGAGCTTCCGGGCGGAGTACAAAGCCACCGGGGGGCGACCGGTTCCAGAAAGCC	1801
QY	1758	GGTCAAGTTCAGGTTGATATCACTACACGAGAGGTTGGGAGAGGCGCAGAAAGGAAACGG	1817
Db	1802	GGTCAAGTTCAGGTTGATATCACTACACGAGAGGTTGGGAGAGGCGCAGAAAGGAAACGG	1861
QY	1818	CATCTACTCGGTCACTTCAACCTGTCTCAGGCGCCACGCGTGTCTCAAGAGGGTGT	1877
Db	1862	CATCTACTCGGTCACTTCAACCTGTCTCAGGCGCCACGCGTGTCTCAAGAGGGTGT	1921
QY	1878	GGAGACCATCCAGGCGCCAGCTGTGAGCACAACAACCCGCTGTGGGCGCCAGCACTTGT	1937
Db	1922	GGAGACCATCCAGGCGCCAGCTGTGAGCACAACAACCCGCTGTGGGCGCCAGCACTTGT	1981
QY	1938	AGACACGAC	1946
Db	1982	AGAACCCCC	1990

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RESULT 13
US-10-283-247-4
; Sequence 4, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NIELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1911
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-283-247-4

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Query Match	84.0%;	Score 1685.2;	DB 15;	Length 1911;
Best Local Similarity	96.2%;	Pred. No. 0;		
Matches 1763;	Conservative	0;	Mismatches 3;	Indels 66;
				Gaps 1;

QY	18	ATGAAAGTGGAGCGGGAGATCGCGATCTTCAAGCTCAATTGAGACACCCCAAGCTCTAAAG	240
Db	1	ATGAAAGTGGAGCGGGAGATCGCGATCTTCAAGCTCAATTGAGACACCCCAAGCTCTAAAG	60
QY	241	CTGCACGACGTTTATGAAAACAAAAAATATTTGTACTGGTGTCTAGAACACAGTCAAGT	300
Db	61	CTGCACGACGTTTATGAAAACAAAAAATATTTGTACTGGTGTCTAGAACACAGTCAAGT	120
QY	301	GGTAGAGCTTTCGACTACCTGCTGATGAAAGAGGAGGCTGACGCTTAAGAGAGGCTCGAAG	360
Db	121	GGTAGAGCTTTCGACTACCTGCTGATGAAAGAGGAGGCTGACGCTTAAGAGAGGCTCGAAG	180
QY	361	TTCTTCGGGAGATCATCTCTGCGCTGGACTTCTGCGACAGCCACTGCATATGCGACAG	420
Db	181	TTCTTCGGGAGATCATCTCTGCGCTGGACTTCTGCGACAGCCACTGCATATGCGACAG	240
QY	421	GATGTGAACCTGAAAACTTCCTCTGAGAGAGAAACAACATCCGCATCGCAGACTTT	480
Db	241	GATGTGAACCTGAAAACTTCCTCTGAGAGAGAAACAACATCCGCATCGCAGACTTT	300
QY	481	GGCATGCGCTCCCTCGACAGTTGCGGCGACAGCTGTTGAGAACCACTGGGTCCCCCAC	540
Db	301	GGCATGCGCTCCCTCGACAGTTGCGGCGACAGCTGTTGAGAACCACTGGGTCCCCCAC	360
QY	541	TAGCCCTGCCCCCGAGGATGATCCGGGAGGAGAAATATACGGCCGGAAAGCGGAGCGTGTG	600
Db	361	TAGCCCTGCCCCCGAGGATGATCCGGGAGGAGAAATATACGGCCGGAAAGCGGAGCGTGTG	420
QY	601	AGCTGCGGCGCTCATCTGTTGCGCTTGCTGGTGGGCGCTCTGCCCTTGACATGACAAAC	660
Db	421	AGCTGCGGCGCTCATCTGTTGCGCTTGCTGGTGGGCGCTCTGCCCTTGACATGACAAAC	480
QY	661	TTTGAGACAGCTGCTGAGAAAGGTAAACCGGGGCGTGTTCCACATGCGGCACTTTATCCG	720
Db	481	TTTGAGACAGCTGCTGAGAAAGGTAAACCGGGGCGTGTTCCACATGCGGCACTTTATCCG	540
QY	721	CCCGACTGCCAGAGTCTGCTACGGGAGCATGATCGAGTGGACGCGCCGACTCAAG	780
Db	541	CCCGACTGCCAGAGTCTGCTACGGGAGCATGATCGAGTGGACGCGCCGACTCAAG	600
QY	781	CTAAGACCATTCAGAAACATATATGATTTAGGGGCAAGATGAGCCCGAACCAAG	840
Db	601	CTAAGACCATTCAGAAACATATATGATTTAGGGGCAAGATGAGCCCGAACCAAG	660
QY	841	CAGCCCATTTCTTCGCAAGGTGCAGATCCGCTGCTGCGCCCTGAGAGCATGACCCC	900
Db	661	CAGCCCATTTCTTCGCAAGGTGCAGATCCGCTGCTGCGCCCTGAGAGCATGACCCC	720
QY	901	GACGTGCTGGAACAGATGCACTCACTGGGCGCTTCGAGACCGCAACACTGCTGAG	960
Db	721	GACGTGCTGGAACAGATGCACTCACTGGGCGCTTCGAGACCGCAACACTGCTGAG	780
QY	961	GACCTGCTGTCCGAGAGAGAACCCAGAGAAATGATTTTACTTCTCTCTGACCCG	1020
Db	781	GACCTGCTGTCCGAGAGAGAACCCAGAGAAATGATTTTACTTCTCTCTGACCCG	840
QY	1021	AAAGAAAGTATCCGAGCCAGAGAGATAGAGACTCGCCCGCCCGGAAAGGATGACCTT	1080
Db	841	AAAGAAAGTATCCGAGCCAGAGAGATAGAGACTCGCCCGCCCGGAAAGGATGACCTT	900
QY	1081	CCCCGGAAGCGTGTGACTCCCGCATGCTGAACCGGACGCGCAAGCGGCGCATGACGC	1140
Db	901	CCCCGGAAGCGTGTGACTCCCGCATGCTGAACCGGACGCGCGCATGACGC	960
QY	1141	AAATTCATGAGAGTGTCTAGCGTGAACGAGCGCGGCTCCCGGATGCTCGCGCGGCGC	1200
Db	961	AAATTCATGAGAGTGTCTAGCGTGAACGAGCGCGGCTCCCGGATGCTCGCGCGGCGC	1020





449 AGGAGAGAGCAATCCGATCGAGACTTTGGCATGGGCTCCCTGAGGTTGGGACA 508  
 494 ATAGAAAAACAATCCGATTCGAGACTTCGGCAATGGCTTCCTGCAAGTGGGAGCA 553  
 509 GCCTGTGGAGACAGCTGTGGGTCCGCCCACTAGCCCTGCGGAGGTGATCCGGGGG 568  
 554 GCCTCTGGAGACAGCTGTGGGTCCGCCCACTATGCTGTGTCAGAGGTGATTAAGGGG 613  
 569 AGAAGTATGACGGCCGGGAGAGCGTGTGGAGCTGCGGCTCATCTGTTGGCTTGG 628  
 614 AAAAATATGATGCGCCGGGAGAGATGTGAGCTGTGAGTGTGATCTCTTGGCTTCG 673  
 629 TGGTGGGGGCTCTGCTCCCTTCAGATGACAACTTGGACAGCTGTGTGAGAGGTGAG 688  
 674 TCGTGGGGGCTCTGCTCCCTTCAGATGACAACTTCGCGCAGCTGTGTGAGAGGTGAG 733  
 689 GGGGCGGTTCACATGCGCACTTTATCCGCGCGACTGCGCAAGTCTGTACGGGGCA 748  
 734 GGGGCGGTTCACATGCGCACTTTATCCGCGCGACTGCGCAAGTCTGTACGGGGCA 793  
 749 TGATCGAGTGTGACGCGCGACGCGGCTCAAGCTAGAGCACTTCAGAAACATATGAT 808  
 794 TGATCGAGTGTGACGCGCGACGCGGCTCAAGCTAGAGCAATTCAGAAACATCTTGGT 853  
 809 ATATAGGGGCAAGATGAGCCCGAACCC-----AGAGAGCCCATTCCTGCAAGGTGC 862  
 854 ACCTAGGCGGAAACAAGAGCCAGACCCGCTGGAGCCAGCCCTGGGCGCGGCTAG 913  
 863 AGATCCGCTGCTGCGCCAGGCTGAGAGACATGCAACCCGCGCTGTGAGCAGATGACAT 922  
 914 CCATGCGGAGCTGCGCACTCAAGAGAGCTGAGACCCCGAGCTCTTGAAGAGATGAT 973  
 923 CACTGCGCTGCTTCGAGACGCGCAACAGCTGTGTGAGAGCACTGTCTGTGAGAGAGAG 982  
 974 CACTGCGCTGCTTCGAGAGCCGCGAGAGGCTGTGATGCGAGCTGCGCAGATGAGAGAG 1033  
 983 ACCAGAGAGAGATGATTTACTTCTCTCTGTGAGCGGAGAGAGAGTACCGAGCAGG 1042  
 1034 ACCAGAGAGAGATGATTTACTTCTCTGTGAGCGGAGAGAGAGTACCGAGCAGG 1093  
 1043 AGATGAGAGAGCTGCGCCCGGAGAGAGATGAGACCTCCCGGAGAGCGTGTGAGCTGCC 1102  
 1094 AGAGCCAGAGACTGCTCCCTCCCGAGATGATGTGACCCCGGAGAGCGTGTGAGATTC 1153  
 1103 CGATCTGAAACCGGACAGCGCAAGCGGCGCCAGAGCAATTCATGAGGTCTCAAGCG 1162  
 1154 CCATGCTGAGCCGTCACGCGAAGGCGGAGCCAGAGCGGAGATCCATGAGATCTTGAAGA 1213  
 1163 TGAAC-----GGAAGGGGGGCTCCCGGAGCTGCGGCGGCGGCGCATTTGAGATGGCC 1213  
 1214 TCACCGATGCCCGGGGTGTGTGCTTCCCTGATCCACCCGAGGCTTTGAGATGGCC 1273  
 1214 AGCAGCGCAGAGGTCTCGGTCACTACGCGGTGCTTCCTGAGCCCTTTCCAGCAGCCAG 1273  
 1274 AGCAGCGCAGAGATTCGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTG 1333  
 1274 TCAGCAGCCCGGGGT----- 1289  
 1334 TAAGCAGCCCAAGAGTCCGCTCTTTTCCCTTTTCCCGAGCGGGGGCTGAGATGAGG 1393  
 1290 ----- 1289  
 1394 CTGAGGCGGGGGCTCCCGCACTTCAAAAGCGAGACGCTGCTTCGCGGGGCCCAAGG 1453  
 1290 -----GACCTCTACCTCTACCAAGGGGAGTTCCTCTCC----- 1326  
 1454 GTGGGGGCGCGGAGAGAGCGCCCGCCCAAGTGGCCCTCCACACCCCTCGCGGCC 1513  
 1327 -----ACCCCAAGGGGAGACCTGTGTGAGCAGCGCA 1357  
 1514 CCCCAGGCTCCCGCGCTCTCTGTGGGGAGACCCCTTGTGACTGCTCTGTGACACCGCCC 1573  
 1358 AGGAGAGCGCGGTGGAGCGCCCAAGCCCAAGCGCCCGCTGCAAGCCC-----AGGCTG 1411

1574 GGGGAGTCCACCGGGAGCCCGGGAGCAACACCAACCCCGGCGGCTGGCTGCG 1633  
 1412 GAGGGTCCCTTGGAGGGCGGGCTCAATCTCCATCAAGAAACATTTCTGGGCTCACCCC 1471  
 1634 GGGGAGCGGCTTGGAGGGTGTCTCAATCTCCATCAAGAAACATTTCTGGGCTCACCCC 1693  
 1472 GCTTCCACCGCGGAAATGCAAGTTCGAGCGCGGAGAGATGTCACACCTGACACCGAG 1531  
 1634 GCTTCCACCGCGGAAATGCAAGTTCGAGCGCGGAGAGATGTCACACCTGACACCGAG 1753  
 1532 AGTCTCCCGAGAGTGGCGAAAGATCTGTGTTGGAACTTCACTGAGCTGAGAAAG 1591  
 1754 AGTCTCCCGAGAGTGGCGAAAGATCTGTGTTGGAACTTCACTGAGCTGAGAAAG 1813  
 1592 AGGAGCAGATCTGTGTGATCAAAAGCAAACTGTGAGCTGATCCATCAAGGCTGACATCG 1651  
 1814 AAGACAAATATTCCTGCTGCTTAAAGACAACTTCTGAGAGATCAAGACATGATCG 1873  
 1652 TGACGCTTCCTGTGTGATTCAGATTCAGCCAGCGGTATCTCCAAACGAGCTTCC 1711  
 1874 TCCATGCTTCTGTGATTCAGATTCAGCCAGCTGATCAGAGTGTCTGTACAGACAGCTTCA 1933  
 1712 GGGCGGATCAAGGCGCAGGGGGGCGCGGCTTCCAAAGCGGTCAAGTTCCAGG 1771  
 1934 GGGCGGATCAAGGCGCAGGGGGGCGCGGCTTCCAAAGCGGTCAAGTTCCAGG 1993  
 1772 TTGATATCACTTACAGAGAGGT-----GGGAGGCGGAGAGAGAG 1813  
 1994 TGACATGATGCTCTCTGATGAGGTCCAGAGCCCTCCCGCGAGCGGAGCGGAGGTG 2053  
 1814 ACGCATCTACTCTGCTACCTTACCTGCTCTGAGGCGCCAGCGGTGCTTCAAGAGG 1873  
 2054 GTGCATCTACTCTGCTACCTTACCTGCTCTGAGGCGCCAGCGGTGCTTCAAGAGG 2113  
 1874 TGGTGAAGACATCCAGGCGCAGGCTGAGAGACACAGCCCGCTGCGGCGGCGACT 1933  
 2114 TGGTGAAGACATCCAGGCGCAGGCTGAGAGACATGAGCAGCCCTCGGTGAGGCGC 2173  
 1934 TGTGAGACCACTTACTG 1952  
 2174 TGGCAGACGAGAGAGCGG 2192

RESULT 15  
 US-10-116-326-1  
 ; Sequence 1, Application US/10116326  
 ; Publication No. US2003016689A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Mathur, Brian  
 ; APPLICANT: Fiddle, Carl Johan  
 ; TITLE OF INVENTION: No. US2003016689A1 Human Kinases and Polynucleotides Encoding  
 ; FILE REFERENCE: Lex-032-USA  
 ; CURRENT APPLICATION NUMBER: US/10/116,326  
 ; PRIOR FILING DATE: 2002-04-04  
 ; PRIOR APPLICATION NUMBER: US 60/282,036  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 2337  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-10-116-326-1

Query Match 48.1%; Score 965; DB 15; Length 2337;  
 Best Local Similarity 70.0%; Pred. No. 4,7e-258;  
 Matches 1484; Conservative 0; Mismatches 440; Indels 195; Gaps 6;

29 GCGACGAGCGGAGATGTTGGGCGCTGACCGGCTGAGAGAGCGCTGGGCAAGGGGAGCA 88  
 74 CCGAGACGCCCAATATGTGGGCGCTTATGCTGAGAGAGCGCTGGGCAAGAGCAAGA 133

QY 89 CAGGTCTGTGAAGCTGGGGGTTCACTGCGTCACTGCGCAGAGGTGGCCATCAAGATCG 148  
 Db 134 CAGGGCTGTGTTAACTGGGGTCCACTGCATCAGGGGTCAAGAGGTGGCCATCAAGATCG 193  
 QY 149 TCAACCTGTGAAGCTCAGCAGGTGGGTGTCTGAAGAAGTGAAGCGAGATCGCATCC 208  
 Db 194 TGAACCGGAGAGCTGTCCGAGTGGGTGTCTGAAGAAGTGAAGCGAGATCGCATCC 253  
 QY 209 TGAAGCTCATTTGAGCACCCTCCAGTCTTAAGTGCACGACCTTTTGAAGAAATAAT 268  
 Db 254 TGAAGCTCATTTGAGCACCCTCCAGTCTTAAGTGCACGACCTTTTGAAGAAATAAT 313  
 QY 269 ATTGTACTGTGTCTGAAGCAAGCTGTCAAGTGTGAGTGTCTTGAAGTCACTGCTGTAAGA 328  
 Db 314 ATTGTACTGTGTCTGAGACAGTGTCCGAGGGGTGAGTGTCTGAGTCACTGCTGTAAGA 373  
 QY 329 AGGAGAGCTGTGACCTCTTAAGAGGCTGTGAAGTCTTCCGAGAGATCATCTGCGCTGG 388  
 Db 374 AGGAGAGCTGTGACCTCTTAAGAGGCTGTGAAGTCTTCCGAGAGATCATCTGCGCTGG 433  
 QY 389 ACTTCTGCAAGCAGCTCTCCATATGACAGAGGATCTGAACCTGAAAACCTGCTGCTGG 448  
 Db 434 ACTTCTGCAAGCAGCTCTCCATATGACAGAGGATCTGAACCTGAAAACCTGCTGCTGG 493  
 QY 449 ACGAGAGAAACAACATCCGATCGCAGACTTTGACATGCGCTCTGACAGTGTGCGACA 508  
 Db 494 ATGAGAAAACAACATCCGATCGCAGACTTTGACATGCGCTCTGACAGTGTGCGACA 553  
 QY 509 GCGCTGTGAGACAGCTGTGGGTGCGCGCCCACTACGCTGCGCGAGAGTATCGGAGG 568  
 Db 554 GCGCTGTGAGACAGCTGTGGGTGCGCGCCCACTACGCTGCGCGAGAGTATCGGAGG 613  
 QY 569 AGAAGTATGACGCGCGAGAGCGAGCGTGTGAGAGCTGCGCGCTCATCTGCTGCTGG 628  
 Db 614 AGAAGTATGAGCGCGCGAGAGCGAGCGTGTGAGAGCTGCGCGCTCATCTGCTGCTGG 673  
 QY 629 TGTGTGGGGCTTCCGCTTGAAGATGACAATTGCGACAGCTGTGAGAGAGTGAAGC 688  
 Db 674 TGTGTGGGGCTTCCGCTTGAAGATGACAATTGCGACAGCTGTGAGAGAGTGAAGC 733  
 QY 689 GGGGCGTGTTCACATGCGCGCACTTTATCCGCGCGAGCTGCGAGAGTGTGCTGAGGAG 748  
 Db 734 GGGGCGTGTTCACATGCGCGCACTTTATCCGCGCGAGCTGCGAGAGTGTGCTGAGGAG 793  
 QY 749 TGAATGAGTGTGAGCGCGCAAGCGCGCTCAAGCTGAGCAGCATTCAGAAACAATGTGT 808  
 Db 794 TGAATGAGTGTGAGCGCGCAAGCGCGCTCAAGCTGAGCAGCATTCAGAAACAATGTGT 853  
 QY 809 ATATAGGGGGCAAGATGAGCGCGAACCC-----AGAGCAGCCCATTCCTCGCAAGTGC 862  
 Db 854 ATATAGGGGGCAAGATGAGCGCGAACCC-----AGAGCAGCCCATTCCTCGCAAGTGC 913  
 QY 863 AGATCGCTGTGCTGCCAGCTGTGAGAGCATCGACCTCGAGCTGTGAGCAGCATGCACT 922  
 Db 914 AGATCGCTGTGCTGCCAGCTGTGAGAGCATCGACCTCGAGCTGTGAGCAGCATGCACT 973  
 QY 923 CACTGGGCTGTTCGAGACCGCAACAAGCTGTGAGCAGCAGTGTGCTGCGAGAGAGAG 982  
 Db 974 CACTGGGCTGTTCGAGACCGCAACAAGCTGTGAGCAGCAGTGTGCTGCGAGAGAGAG 1033  
 QY 983 ACGAGAGAAAGATATTACTTCTCTCTGAGCCGAGAAAGAAAGTACCGAGCGAG 1042  
 Db 1034 ACGAGAGAAAGATATTACTTCTCTCTGAGCCGAGAAAGAAAGTACCGAGCGAG 1093  
 QY 1043 AGGATGAGAGCTTGTGCGCGCGAGAGAGATAGCCTTCCGCGAGAGCTGTGAGATCCC 1102  
 Db 1094 AGGATGAGAGCTTGTGCGCGCGAGAGAGATAGCCTTCCGCGAGAGCTGTGAGATCCC 1153  
 QY 1103 CGATGTGAAACCGGACGAGCAGCGCGAGCGCGAGAGCAATTCATGAGAGTGTGAGCG 1162  
 Db 1154 CGATGTGAAACCGGACGAGCAGCGCGAGCGCGAGAGCAATTCATGAGAGTGTGAGCG 1213

QY 1163 TGAC-----GACCGCGGCTTCCCGGCTGCGCGGCGGCGCATTTGAGATGGCCC 1213  
 Db 1214 TCACGAGATCGCGGAGGTGTGTGCTTCCCTGTGACCAACCGAGCGCTTGAAGATGGCCC 1273  
 QY 1214 AGCAGGCTCAAGGCTTGTGTGCTATGACGCTGTGCTTCAAGAGCGGCGAC 1273  
 Db 1274 AGCAGGCTCAAGGCTTGTGTGCTATGACGCTGTGCTTCAAGAGCGGCGAC 1333  
 QY 1274 TCAGAGCGCGCGGCT-----ACCCCAAGGGGACACTGTGCAACGCGCA 1289  
 Db 1334 TGAAGAGCCCAAGAGATCCGCTCTTTCTTTTCAACCGAGCGCGGAGCTGAGATGAGG 1393  
 QY 1290 ----- 1289  
 Db 1394 CTCGAGCGGAGGCTCCCGCATTCGAAACGAGAGCTGCTTCTGCGGCGCCGAGG 1453  
 QY 1290 -----GACCCCTGACCCCTGACCAAGAGGAGGAGTCCCTCC----- 1326  
 Db 1454 GTGGGGGCGCGGAGAGAGCGCCCGCCGAGAGCGCTGCAACCCCTGCGCGGCG 1513  
 QY 1327 -----ACCCCAAGGGGACACTGTGCAACGCGCA 1357  
 Db 1514 CCGCAGGCTCCCGGCTCTCTGTGCGGAGACCCCTTGAAGTCTGCTGCAACGCGCC 1573  
 QY 1358 AGGAGAGCGCGGCTGAGACGCGCAACCGCAAGCGCGCGCGCGCGCG-----AGCGTGG 1411  
 Db 1574 GCGCGAGTCCACGAGAGCCTCGGAGAGACACACACCGCGCGCGCGCGCGCGCTG 1633  
 QY 1412 GAGGAGTGCCTGTGAGAGCGCGGCTCACTTCATCAAGAAACAGTTTGTGGCTCACCC 1471  
 Db 1634 GGGGAGCGCGCTGAGAGAGTGTGTCTCAATCTCAACCGCAACAGTTTGTGGCTCACCC 1693  
 QY 1412 GCTTCCACCGCGGAACTGCAAGTTTCCAGCGCGGAGAGATGTCCAACTGACACAG 1531  
 Db 1694 GCTTCCACCGCGGAACTGCAAGTTTCCAGCGCGGAGAGATGTCCAACTGACACAG 1753  
 QY 1532 AGTGCCTCCCGAGAGCTGCGAGAGAGTCTGTGTGAGAACTTTCAGAGCTGTGAGAG 1591  
 Db 1754 AGTGCCTCCCGAGAGCTGCGAGAGAGTCTGTGTGAGAACTTTCAGAGCTGTGAGAG 1813  
 QY 1592 AGAGCAGATTTGTGTGTATCAAGAACAACTCTGAGAGTCCATCAAGCTGTGACATG 1651  
 Db 1814 AAGAACAAATTTCTGTGTGTATCAAGAACAACTCTGAGAGTCCATCAAGCTGTGACATG 1873  
 QY 1652 TGAAGCTTCTGTGTGTATCCAGTCTCAGCGCACAGCTCATCTCCAAACGAGCTTCC 1711  
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 QY 1712 GGGCGAGTCAAGGCTCAGGCGGCGAGCGCTGTGTGAGAGCGGCTCAAGTTCAGG 1771  
 Db 1934 GGGCGAGTCAAGGCTCAGGCGGCGAGCGCTGTGTGAGAGCGGCTCAAGTTCAGG 1993  
 QY 1772 TTGATATCACTCAACGAGAGGT-----GGGAGGCGCAGAGAGAG 1813  
 Db 1994 TGAAGATAGCTCTCTGTGAGAGTCCAGAGCGCTTCCCGCAGCGGAGCGAGAGTGT 2053  
 QY 1814 ACGGATCTACTCTGTGACCTTCAACCTGCTCTGAGCGCGCGAGCTTCAAGAGG 1873  
 Db 2054 GTGGCATCTACTCTGTGACCTTCAACCTGCTCTGAGCGCGCGAGCTTCAAGAGG 2113  
 QY 1874 TGTGTGAGAACATTCAGGCGCGAGCTGTGAGCAACAGAGCGCGCGCGCGAGCACT 1933  
 Db 2114 TGTGTGAGAACATTCAGGCGCGAGCTGTGAGCAACAGAGCGCGCGCGCGAGCACT 2173  
 QY 1934 TGTCAAGCAGCACTAAGT 1952  
 Db 2174 TGCAGAGAGAGAGAGCG 2192

Search completed: August 5, 2004, 10:23:16  
 Job time : 668 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 10:21:35 ; Search time 19 Seconds  
(without alignments)

1815.060 Million cell updates/sec

Title: US-10-054-579-2

Perfect score: 3497  
Sequence: 1 MTSTGDKGAGHQAQYVGYR.....TNCMEMTGRLSKGIIPRS 668

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/2/1aa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUS COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3497	100.0	668	US-09-930-181-2	Sequence 2, Appl1
2	3028	86.6	585	US-09-930-181-4	Sequence 4, Appl1
3	3015	86.2	603	US-09-930-181-17	Sequence 17, Appl1
4	796.5	22.8	745	US-09-523-849-16	Sequence 16, Appl1
5	793.5	22.7	724	US-09-984-890-2	Sequence 2, Appl1
6	792.5	22.7	722	US-09-984-890-4	Sequence 4, Appl1
7	790.5	22.6	722	US-08-817-832B-32	Sequence 32, Appl1
8	768.5	22.0	729	US-08-677-298-2	Sequence 2, Appl1
9	768.5	22.0	729	US-09-523-849-33	Sequence 33, Appl1
10	764.5	21.9	793	US-09-523-849-32	Sequence 32, Appl1
11	749	21.4	776	US-09-523-849-34	Sequence 34, Appl1
12	749	21.4	779	US-08-817-832B-31	Sequence 31, Appl1
13	740	21.2	1203	US-09-799-875-5	Sequence 5, Appl1
14	729.5	20.9	552	US-08-557-006C-40	Sequence 40, Appl1
15	720.5	20.6	633	US-08-557-006C-43	Sequence 43, Appl1
16	718.5	20.5	345	US-09-101-146-1	Sequence 1, Appl1
17	694.5	19.9	257	US-09-101-146-6	Sequence 6, Appl1
18	681	19.5	257	US-07-857-224B-25	Sequence 25, Appl1
19	680	19.4	149	US-09-930-181-18	Sequence 18, Appl1
20	670.5	19.2	634	US-09-523-849-35	Sequence 35, Appl1
21	599.5	17.1	601	US-09-579-664B-11	Sequence 11, Appl1
22	523	15.0	290	US-09-734-673-4	Sequence 4, Appl1
23	523	15.0	334	US-09-523-849-31	Sequence 31, Appl1
24	520.5	14.9	252	US-07-857-224B-26	Sequence 26, Appl1
25	515.5	14.7	436	US-09-734-673-2	Sequence 2, Appl1
26	515.5	14.7	436	US-09-523-849-2	Sequence 2, Appl1
27	506.5	14.5	260	US-07-857-224B-27	Sequence 27, Appl1

28	501	14.3	353	3	US-08-688-988-31	Sequence 31, Appl1
29	491.5	14.1	556	4	US-09-800-960-4	Sequence 4, Appl1
30	491.5	14.1	556	4	US-10-096-960-4	Sequence 4, Appl1
31	490	14.0	363	3	US-08-688-988-30	Sequence 30, Appl1
32	488.5	14.0	260	2	US-07-857-224B-28	Sequence 28, Appl1
33	488	14.0	504	4	US-09-554-726A-10	Sequence 10, Appl1
34	485	13.9	339	3	US-08-688-988-33	Sequence 33, Appl1
35	485	13.9	351	3	US-08-688-988-28	Sequence 28, Appl1
36	485	13.9	565	4	US-09-800-960-2	Sequence 2, Appl1
37	485	13.9	565	4	US-10-096-960-2	Sequence 2, Appl1
38	481	13.8	354	3	US-08-688-988-29	Sequence 29, Appl1
39	471.5	13.5	359	3	US-08-688-988-32	Sequence 32, Appl1
40	470.5	13.5	455	4	US-09-554-726A-7	Sequence 7, Appl1
41	469.5	13.4	1037	4	US-09-428-711A-21	Sequence 21, Appl1
42	467.5	13.4	339	3	US-08-688-988-2	Sequence 2, Appl1
43	466.5	13.3	295	2	US-07-951-715A-23	Sequence 23, Appl1
44	466.5	13.3	295	2	US-08-459-448A-23	Sequence 23, Appl1
45	466.5	13.3	295	3	US-08-459-595A-23	Sequence 23, Appl1

## ALIGNMENTS

RESULT 1  
US-09-930-181-2  
; Sequence 2, Application US/09930181  
; Patent No. 6455292  
; GENERAL INFORMATION:  
; APPLICANT: Origene Technologies  
; TITLE OF INVENTION: Full-length Serine Protein Kinase In Brain and Pancreas  
; FILE REFERENCE: 16U 101 V1  
; CURRENT FILING DATE: 2001-08-16  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 2  
; LENGTH: 668  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-930-181-2

Query Match 100.0%; Score 3497; DB 4; Length 668;  
Best Local Similarity 100.0%; Pred. No. 1.96-251;  
Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTSTGDKGAGHQAQYVGYRLEKTLGKGTGVKVCVTCQKAIKIVREKLSSTL	60
DB	1	MTSTGDKGAGHQAQYVGYRLEKTLGKGTGVKVCVTCQKAIKIVREKLSSTL	60
QY	61	MKVERIALTKLIEHPVYKLDHYENKKYLYLVLEHSGELFDYLVKGRITPREARK	120
DB	61	MKVERIALTKLIEHPVYKLDHYENKKYLYLVLEHSGELFDYLVKGRITPREARK	120
QY	121	PFQRIISALDFGSHSICRDLKPENLIDEXNNIRIADFGASIQVGDLSLETSCGSPH	180
DB	121	PFQRIISALDFGSHSICRDLKPENLIDEXNNIRIADFGASIQVGDLSLETSCGSPH	180
QY	181	YACPEYIREKXDKGRADVWSCGVLPFLLVGLPFDDNNLRQLEKYGKGFVHPFP	240
DB	181	YACPEYIREKXDKGRADVWSCGVLPFLLVGLPFDDNNLRQLEKYGKGFVHPFP	240
QY	241	PCQSLIRGMIIVDARRLTLLEHIOKHIWYIGKNEPEEOPIPRKVOIRSLPSLEIDP	300
DB	241	PCQSLIRGMIIVDARRLTLLEHIOKHIWYIGKNEPEEOPIPRKVOIRSLPSLEIDP	300
QY	301	DVLDSHSGICPRDRKYLQDLISEENOEKKIYELLDRKRYSOEDEDLPRENEIDP	360
DB	301	DVLDSHSGICPRDRKYLQDLISEENOEKKIYELLDRKRYSOEDEDLPRENEIDP	360
QY	361	PRKRVDSPLNINHGKRRPERKSMENVLYVTDGSGPYPARRAIEMAGHGRSISGASGL	420
DB	361	PRKRVDSPLNINHGKRRPERKSMENVLYVTDGSGPYPARRAIEMAGHGRSISGASGL	420

QY 421 STPLSPSPVTPHPSPGSPPLPTPKGTQVHTPKESPAGTNPPTPSSSVGVPMARLN 480  
 DB 421 STPLSPSPVTPHPSPGSPPLPTPKGTQVHTPKESPAGTNPPTPSSSVGVPMARLN 480  
 QY 481 SIKNSFLGSPRHRKQLQVPTPEEMSNLTPESSPELAKKSMFGNFISLEKEBOIFVVIKQ 540  
 DB 481 SIKNSFLGSPRHRKQLQVPTPEEMSNLTPESSPELAKKSMFGNFISLEKEBOIFVVIKQ 540  
 QY 541 KPLSLIKADIHARLSIPSLSHSVISQTSFPAEYKATGAPVPOKPKFQVDITTEGGE 600  
 DB 541 KPLSLIKADIHARLSIPSLSHSVISQTSFPAEYKATGAPVPOKPKFQVDITTEGGE 600  
 QY 601 AOKENGIVSVFTLLSGSPRRFKRQVETIOAQLLSTHDPAPAOHLSDTNMCMEMTGRLS 660  
 DB 601 AOKENGIVSVFTLLSGSPRRFKRQVETIOAQLLSTHDPAPAOHLSDTNMCMEMTGRLS 660  
 QY 661 KCGIIPKS 668  
 DB 661 KCGIIPKS 668

## RESULT 2

US-09-930-181-4  
 ; Sequence 4, Application US/09930181  
 ; Patent No. 6455292  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Origene Technologies  
 ; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas  
 ; FILE REFERENCE: 16U 101 V1  
 ; CURRENT APPLICATION NUMBER: US/09/930,181  
 ; CURRENT FILING DATE: 2001-08-16  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: Patent version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 585  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-930-181-4

## Query Match

86.6%; Score 3028; DB 4; Length 585;

Best Local Similarity 100.0%; Pred. No. 1e-216;

Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 YLVLEHVSQGLFPIYLVKKGRLTPKRAKFPROIISALDCHSHICHRDLKXENLLDE 151  
 DB 9 YLVLEHVSQGLFPIYLVKKGRLTPKRAKFPROIISALDCHSHICHRDLKXENLLDE 68  
 QY 152 KNNIRIADFGMASLQVDSILETSCGSPHYACPEVIRGEKXDGKADVMSGVILPALLY 211  
 DB 69 KNNIRIADFGMASLQVDSILETSCGSPHYACPEVIRGEKXDGKADVMSGVILPALLY 128  
 QY 212 GALPDDNNLRQLEKXKRGVFMHPHTIPDCCOSLLRGMEVDAARLTLEHTOKHIIWYI 271  
 DB 129 GALPDDNNLRQLEKXKRGVFMHPHTIPDCCOSLLRGMEVDAARLTLEHTOKHIIWYI 188  
 QY 272 GGNKEPEPEQPIPRKVOIRSLPSLEDIDPVLDSMHSIGCFRDNRKLLQDLSEENQEX 311  
 DB 189 GGNKEPEPEQPIPRKVOIRSLPSLEDIDPVLDSMHSIGCFRDNRKLLQDLSEENQEX 248  
 QY 332 MIYLLLDKXERYSOEDEDLPKNEIDPPKRVDSMLNRAGKRRPERKSMVLSVTG 391  
 DB 249 MIYLLLDKXERYSOEDEDLPKNEIDPPKRVDSMLNRAGKRRPERKSMVLSVTG 308  
 QY 392 GSPPARRAIEMAHQGRSRSISGASGLSTSPASRVTPHPSPRGSPLPTPKGTQVHT 451  
 DB 309 GSPPARRAIEMAHQGRSRSISGASGLSTSPASRVTPHPSPRGSPLPTPKGTQVHT 368  
 QY 452 PKESPAGTNPPTPSSSVGVPMARLNSIKNSFLGSPRHRKQLQVPTPEEMSNLTPE 511  
 DB 369 PKESPAGTNPPTPSSSVGVPMARLNSIKNSFLGSPRHRKQLQVPTPEEMSNLTPE 428  
 QY 512 SSPELAKKSMFGNFISLEKEBOIFVVIKDKPLSSIKADIHARLSIPSLSHSVISQTSF 571

DB 429 SSPELAKKSMFGNFISLEKEBOIFVVIKDKPLSSIKADIHARLSIPSLSHSVISQTSF 488  
 QY 572 AEVKATGGPAVOKRVKQVQDITTEGGEAOKENGIVSVFTLLSGSPRRFKRQVETIOA 631  
 DB 489 AEVKATGGPAVOKRVKQVQDITTEGGEAOKENGIVSVFTLLSGSPRRFKRQVETIOA 548  
 QY 632 QLLSTHDPAPAOHLSDTNMCMEMTGRLSKCGIIPKS 668  
 DB 549 QLLSTHDPAPAOHLSDTNMCMEMTGRLSKCGIIPKS 585

## RESULT 3

US-09-930-181-17  
 ; Sequence 17, Application US/09930181  
 ; Patent No. 6455292  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Origene Technologies  
 ; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas  
 ; FILE REFERENCE: 16U 101 V1  
 ; CURRENT APPLICATION NUMBER: US/09/930,181  
 ; CURRENT FILING DATE: 2001-08-16  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: Patent version 3.0  
 ; SEQ ID NO 17  
 ; LENGTH: 603  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-930-181-17

## Query Match

86.2%; Score 3015; DB 4; Length 603;

Best Local Similarity 99.7%; Pred. No. 9.9e-216;

Matches 574; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 72 LIENHPVLKLDVYENKRYLYLVLEHVSQGLFPIYLVKKGRLTPKRAKFPROIISALDF 131  
 DB 1 LIENHPVLKLDVYENKRYLYLVLEHVSQGLFPIYLVKKGRLTPKRAKFPROIISALDF 60  
 QY 132 CHSHICHRDLKXENLLDEKNNIRIADFGMASLQVDSILETSCGSPHYACPEVIRGEK 191  
 DB 61 CHSHICHRDLKXENLLDEKNNIRIADFGMASLQVDSILETSCGSPHYACPEVIRGEK 120  
 QY 192 YDGRKADVMSGVILPALLYVAGLPPDDNNLRQLEKXKRGVFMHPHTIPDCCOSLLRGMS 251  
 DB 121 YDGRKADVMSGVILPALLYVAGLPPDDNNLRQLEKXKRGVFMHPHTIPDCCOSLLRGMS 180  
 QY 252 EYDARRLTLEHTOKHIIWYIIGKNEPEPEQPIPRKVOIRSLPSLEDIDPVLDSMHSIGC 311  
 DB 181 EYDARRLTLEHTOKHIIWYIIGKNEPEPEQPIPRKVOIRSLPSLEDIDPVLDSMHSIGC 240  
 QY 312 FDRNRKLLQDLSEENQEXMIYLLLDKXERYSOEDEDLPKNEIDPPKRVDSMPLN 371  
 DB 241 FDRNRKLLQDLSEENQEXMIYLLLDKXERYSOEDEDLPKNEIDPPKRVDSMPLN 300  
 QY 372 RHGKRRPERKSMVLSVTGSSPVPARRAIEMAHQGRSRSISGASGLSTSPASRVTP 431  
 DB 301 RHGKRRPERKSMVLSVTGSSPVPARRAIEMAHQGRSRSISGASGLSTSPASRVTP 360  
 QY 432 PHPSRGSPLPTPKGTQVHTPKESPAGTNPPTPSSSVGVPMARLNSIKNSFLGSPR 491  
 DB 361 PHPSRGSPLPTPKGTQVHTPKESPAGTNPPTPSSSVGVPMARLNSIKNSFLGSPR 420  
 QY 492 FHRRLQVPTPEEMSNLTPESSPELAKKSMFGNFISLEKEBOIFVVIKDXPLSSIKADI 551  
 DB 421 FHRRLQVPTPEEMSNLTPESSPELAKKSMFGNFISLEKEBOIFVVIKDXPLSSIKADI 480  
 QY 552 HAFSLIPSLSHSVISQTSFPAEYKATGAPVPOKPKFQVDITTEGGEAOKENGIVSVT 611  
 DB 481 HAFSLIPSLSHSVISQTSFPAEYKATGAPVPOKPKFQVDITTEGGEAOKENGIVSVT 540  
 QY 612 FTLLSGSPRRFKRQVETIOAQLLSTHDPAPAOHLSD 647  
 DB 541 FTLLSGSPRRFKRQVETIOAQLLSTHDPAPAOHLSD 576

```

RESULT 4
US-09-523-849-36
; Sequence 36, Application US/09523849
; Patent No. 6438561
; GENERAL INFORMATION:
; APPLICANT: Bardman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scaccheri, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 36
; LENGTH: 745
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Genbank Accession No. 6458561 g1749794
US-09-523-849-36

Query Match      22.8%; Score 796.5; DB 4; Length 745;
Best Local Similarity 29.1%; Pred. No. 6,4e-51;
Matches 224; Conservative 120; Mismatches 243; Indels 183; Gaps 21;

QY 10 AOHAYVGYPRLEKTLGKQGTGLVKGVCVTCQKVAIKIVNREKLSSEVLMKVEREIAI 69
DB 11 ADEQPHIGNYRLTKTIKGNPAKVLARHILTGKEVAVKIIDTQINSSSLQKLFREVR 70
QY 70 LKLEHNYLKLHVNENKYLIVLEHVSGLLEFDLYVKKGRLLPPEAKRFROIIASL 129
DB 71 MKVNHFNIVLFEVITEKTLVMEYASGGEVFDLYVAGRMKEKARAKRQIVSAV 130
QY 130 DFCHSHSICHRDLKRENILDEKNNIRIADFGMASLQVGSLLFETSCSPHYACEVIRG 189
DB 131 QYCHQKFIYHRDLKAKENLLDADNMKIKIADFGSNEFTFGNKLDTCGSPYAAPELFG 190
QY 190 EKYDGRKADVWSCGVIIFALLVGLPDDNLRQLLEKYKRGVFMHFIIPDCQSLRG 249
DB 191 KKYDGEVDVWSLGVIIYTLVSGSLPFDQNLKELREVRVLRKRYIFPYMSTDCENLLK 250
QY 250 MIEVDARLTLLEHIQKHIWYIGKNEPEPEQPIPRKQIRSLPSELDIDPVLDSMSTL 309
DB 251 FLINPSKRGTLQIMKDRMNVGHEDE-----LKPYEPLPYK--DPRTELMSM 302
QY 310 GCFRDNKLLQDLSEENOEKTYFLILDRKERYPSQEDBDLPPEINID----- 359
DB 303 GYTRER-----IQDSLVGRVNEVMATYLLIGYKSELEGGDTITLKPRPSADLTNSAQF 359
QY 360 -----PBRKRVVS-----PMLNRHGK-----RRPE-----RKS----- 383
DB 360 HKVORSVSANPKORRPSDQAPALFTNSYSKKTQSNNAENKREERREGSKRATYK 419
QY 384 -----EVLSTDG-----GSFVPARRALEMA--CHGQRSSISG--A 416
DB 420 PASPLGLERKKTPTPTSTNSVLSTSTRNSPDLBRASIQGASIQNGKDSLMPSSRA 479
QY 417 SSGISTSLSPRTPH-----PSPRGSLPPEKTPVHTPESPA-- 457
DB 480 STASASVSAARPPROHQKMSASVHNPYASGLPPTESNCEVPSPSTAPORVYASAS 539
QY 458 -----GTNPPT-----PPSSSVGVGVPMARLNS 481
DB 540 NISSSGGAPDRTPRGVSSRSTFHAGQLRQVDOQLPYGVTPASVSGHSGGRGASG 599
QY 482 IKNSFLGSPRFRKRLQVP--TPREMSNLTP-----SSPELAKSM--FG 523

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DB 600 IFSKF--TSKFRRLNBPESKDRVETLRPHVVSQGNDEKEBEFRKAPSLRFTSMK 657
QY 524 NFISLEKEQJFVVKDKPLSSIKADIYHAFILPSLSHVISQTSFPAEYKATGAPAVE 583
DB 658 TTSSMEPEMREIRKULDANSQSELEKXMLL--CHGTPGHEDF----- 702
QY 584 QKPYKQVDITYTEGGAQKENGIVSYFTLLISGSRFRKRVETIQOAL 633
DB 703 ---VQMEWEC-----KLPRLSLNGVFRKRIISGTSMVAKXIASKXIANEL 743

RESULT 5
US-09-984-890-2
; Sequence 2, Application US/09984890
; Patent No. 6492156
; GENERAL INFORMATION:
; APPLICANT: VAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01306
; CURRENT APPLICATION NUMBER: US/09/984,890
; CURRENT FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 724
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-984-890-2

Query Match      22.7%; Score 793.5; DB 4; Length 724;
Best Local Similarity 29.8%; Pred. No. 1e-50;
Matches 216; Conservative 115; Mismatches 248; Indels 145; Gaps 19;

QY 10 AOHAYVGYPRLEKTLGKQGTGLVKGVCVTCQKVAIKIVNREKLSSEVLMKVEREIAI 69
DB 44 ADEQPHIGNYRLTKTIKGNPAKVLARHILTGKEVAVKIIDTQINSSSLQKLFREVR 103
QY 70 LKLEHNYLKLHVNENKYLIVLEHVSGLLEFDLYVKKGRLLPPEAKRFROIIASL 129
DB 104 MKVNHFNIVLFEVITEKTLVMEYASGGEVFDLYVAGRMKEKARAKRQIVSAV 163
QY 130 DFCHSHSICHRDLKRENILDEKNNIRIADFGMASLQVGSLLFETSCSPHYACEVIRG 189
DB 164 QYCHQKFIYHRDLKAKENLLDADNMKIKIADFGSNEFTFGNKLDTCGSPYAAPELFG 223
QY 190 EKYDGRKADVWSCGVIIFALLVGLPDDNLRQLLEKYKRGVFMHFIIPDCQSLRG 249
DB 224 KKYDGEVDVWSLGVIIYTLVSGSLPFDQNLKELREVRVLRKRYIFPYMSTDCENLLK 283
QY 250 MIEVDARLTLLEHIQKHIWYIGKNEPEPEQPIPRKQIRSLPSELDIDPVLDSMSTL 309
DB 284 FLINPSKRGTLQIMKDRMNVGHEDE-----LKPYEPLPYK--DPRTELMSM 335
QY 310 GCFRDNKLLQDLSEENOEKTYFLILDRKERYPSQEDBDLPPEINIDPPEKRVDS 368
DB 336 GYTRER-----IQDSLVGRVNEVMATYLLIGYKSELEGGDTITLKPRPSADLTNSA 392
QY 369 --MLNRHGKRRPBRKRVESLSTVDGSPVPA-----RALEMAQHQRSS 412
DB 393 HKVORSVSANPKORRPS--DQAPALFTNSYSKKTQSNNAENKREERREGSKR 448
QY 413 ISGASGLSTSP--LSRPVTPHPS-----PRGSP----- 441
DB 449 ---TAKYASPLPGLERKKTPTPTSTNSVLSTSTRNSPDLBRASIQGASIQNGK 504
QY 442 PTPKGTVPHTPK--ESPAGTPNPT-----PPSSSVGVGVPMARLNS 467
DB 505 TAPQRPVVASPSAHNISSSGAPDRTPRGVSSRSTFHAGQLRQVDOQLPYGVTPAS 564
QY 468 PSYGVPMARLNSINSLGSPRFRKRLQVP--TPREMSNLTP-----SSPELAKSM--FG 510

```

Db 565 PSCHSGCRGASGSISFISKF--TSKFTVRKNINBPESKDRVETLAPHHVGGSGNDKEKEFR 622  
Qy 511 ESSBELAKGSM-FGNFISLEKEQIFVIVIKDKPLSISIKADIYAHFISPSLSHSVISQTS 569  
Db 623 EAKRSRLFTWSMKTTSSMEPNEMRRIKRYLDANSQSSEIHERMYML--CMHGTPGHD 680  
Qy 570 FRAHYKATGPAVQKRVQVODITYTEGGEAQKENGIVSYTTLISGSPRRKRVETI 629  
Db 681 F-----VQWEMEVC-----KLPRSLNGVRFKRISGTSMAFKNIASKI 718  
Qy 630 QAOCL 633  
Db 719 ANEL 722

RESULT 6  
US-09-984-890-4  
; Sequence 4, Application US/09984890  
; Patent No. 6492156  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001306  
; CURRENT APPLICATION NUMBER: US/09/984,890  
; CURRENT FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO: 4  
; LENGTH: 722  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-984-890-4

Query Match 22.7%; Score 792.5; DB 4; Length 722;  
Best Local Similarity 30.2%; Pred. No. 1.2e-50;  
Matches 217; Conservative 115; Mismatches 251; Indels 135; Gaps 18;

Qy 10 AQHAYGVPYRIEKTIGGQGTGLVGHVCTGCKVAIKIVNREKLSSEVLMKVEREIAI 69  
Db 44 ADEPHIGNRRLKTIKGNFAKYLARHILITGEVAVKIIDKQLNSSLQKLFREYRI 103  
Qy 70 LKLIHPHVLKLDVYENKRYLYVLEHVSGBELFDYLVKKGRLTPREARKFRQIISAL 129  
Db 104 MKVLNHPNIVLFEVIEETKTLVYVMEYASGGEVFDYLVHAGMKEKEARAKFRQIVSAV 163  
Qy 130 DFGSHSICRDLKPEENILDEKKNIRIADFGMASLQVGSILETSGSPHYACPEVIRG 189  
Db 164 QYCHQKTIVRHDLKAEENILADAMNLIKADFGFSNEFTFGKLDITFGSPHYAABELFQ 223  
Qy 190 EKYDGRKADVWSCGVIIFALLVGALEPDDNLRQLLEKVRGVFHMHPFIIPDCQSLRG 249  
Db 224 KKYDGPEDVWMSLVIIYTLVSGSLPFDGQNLKELRERVLRGKXRIIPYVSTDCENILKK 283  
Qy 250 MIEVDARLRLTHIIGHIYIGKNEPEEQPIPRVQYRSIPLSEIDEDVDLDMHSL 309  
Db 284 FLINPSKRGTLLEIMDRMNVGHEDD-----LPEYVEPLPDYK--DPRKTELWSTW 335  
Qy 310 GCFPRKRLQDLSEENOEKMIYFLLDRKERYPSODEDLPFRNEID----- 359  
Db 336 GYTRHE--IDSLVGQRVYVAVATYLLGVKSELEGDITTLKPRASADLTNSAPSPS 392  
Qy 360 -----PPKRVDS-----PMANRHK-----RPE-----RKSMEVLSYND 390  
Db 393 HKVORSVANKQKORSSDOAVPALFTNSYSKKTQSNNAENKSPPEEBTGKASSTAKVP- 451  
Qy 391 GGSFVPAARAITEMOHQGRSISIGASSGLSTPL-----SSPVTPEH 433  
Db 452 -ASLPLGIDRKKTPTPTSTNSVLSTNRRGNSBLDRASLQGASTONGSDSTAPGRVPI 510  
Qy 434 PSPGSGSLPFPKGTPTVHPKXESPAGT-----PNPTPSSPSVGV 473

Db 511 ASPSAHNISSSSGAPDRF--NFPQVSSRSTFHAGQLQVQRDQONLFFGVTPASPQSHSQ 568  
Qy 474 PWRALNISTKNSFISGPRFRKQLQV-TPBEMNLTP-----ESSPEL 516  
Db 569 GRGAGSGSIFSKF--TSKFTVRKNINBPESKDRVETLAPHHVGGGTDKKEBFEARPRS 626  
Qy 517 AKGSM-FGNFISLEKEQIFVIVIKDKPLSISIKADIYAHFISPSLSHSVISQTSFPAEYK 575  
Db 627 LRFTWSMKTTSSMEPNEMRRIKRYLDANSQSSEIHERMYML--CVHGTPGHEMF----- 679  
Qy 576 ATGPAVQKRVQVODITYTEGGEAQKENGIVSYTTLISGSPRRKRVETI 633  
Db 680 -----VQWEMEVC-----KLPRSLNGVRFKRISGTSMAFKNIASKIANEL 720

RESULT 7  
US-08-817-832B-32  
; Sequence 32, Application US/08817832B  
; Patent No. 6579691  
; GENERAL INFORMATION:  
; APPLICANT: MANDELKOM, Eckhard, et al.  
; TITLE OF INVENTION: No. 6579691e1 Protein Kinase (NPK-110)  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 S. Wacker Drive, 6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: US  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/817,832B  
; FILING DATE: 28-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP95/04258  
; FILING DATE: 30-OCT-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94 11 7122.5  
; FILING DATE: 28-OCT-1994  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 722 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-817-832B-32

Query Match 22.6%; Score 790.5; DB 4; Length 722;  
Best Local Similarity 30.2%; Pred. No. 1.7e-50;  
Matches 217; Conservative 115; Mismatches 251; Indels 135; Gaps 18;

Qy 10 AQHAYGVPYRIEKTIGGQGTGLVGHVCTGCKVAIKIVNREKLSSEVLMKVEREIAI 69  
Db 44 ADEPHIGNRRLKTIKGNFAKYLARHILITGEVAVKIIDKQLNSSLQKLFREYRI 103  
Qy 70 LKLIHPHVLKLDVYENKRYLYVLEHVSGBELFDYLVKKGRLTPREARKFRQIISAL 129  
Db 104 MKVLNHPNIVLFEVIEETKTLVYVMEYASGGEVFDYLVHAGMKEKEARAKFRQIVSAV 163  
Qy 130 DFGSHSICRDLKPEENILDEKKNIRIADFGMASLQVGSILETSGSPHYACPEVIRG 189  
Db 164 QYCHQKTIVRHDLKAEENILADAMNLIKADFGFSNEFTFGKLDITFGSPHYAABELFQ 223  
Qy 190 EKYDGRKADVWSCGVIIFALLVGALEPDDNLRQLLEKVRGVFHMHPFIIPDCQSLRG 249  
Db 224 KKYDGPEDVWMSLVIIYTLVSGSLPFDGQNLKELRERVLRGKXRIIPYVSTDCENILKK 283

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QY 250 MIEVDARRLTLEHIOKHIVYIGKNEPEEQPIPRKQVIRSLPSLEDDIDPVLDSMHSI 309
DB 284 FLINPFRKGLTLEIMKIDRMWNVGHEDE-----LKPVEPLPDYK--DPRTELWVSK 335
QY 310 GCFDRNKLLODLSEBNOEKMIYFLILDRKERYPEQDEDLPRNEID----- 359
DB 336 GYTRFE---IQDSLVGRNVEWATYLLGLYKSELEGDITILKPRSAULTMSASPS 392
QY 360 -----PPRKRVDS-----PVLNRHK-----RPE---RKSNEVLSTVD 390
DB 393 HKYQSVSNAPKQRRSSDOAVPALPTNSYSKTKQSNMAENKRPPEBTGRKASTAKVP- 451
QY 391 GGSVPARARAIEMAHQGRSRISGASSGLSTPL-----SSPRVTPH 433
DB 452 -ASPLPGLDRKKTTPPTSTNSVLTSTNRSNSPLDRASLGQASTONGKSTAPQRPVY 510
QY 434 PSPRGSPLPTPKCTPVHTPKESPAGT-----ENPTPSSPSVGVY 473
DB 511 ASPAHNIISSSGAPDRT--NFRGVSSRSTFHAGLRQVDOONLFFGVTPASPSGHSQ 568
QY 474 PWRRLNSIKNSFGSRFRHKLQVP--TPEMKNLTP-----ESPEL 516
DB 569 GRKPSGSIFSKF--TSKPRRNINPEESKQVETLEPHVVGCGGTDKEKEPREAKPRS 626
QY 517 AKKSN-FGNFISLEKEBQIFVYIKDKPLSSIKADIVAHFLISLSHSVISQTSFRAEYK 575
DB 627 LRFWMSKTTSSMPEMMEIRKVLANSQSESLHRWYLL--CVHTGTHENF----- 679
QY 576 ATGSPAVFQKPKQVDITYTEGGEAQKNGIYVTTLSGPRRRKRVETIQOL 633
DB 680 -----VQWEMEVC-----KLPRLSLNGVRKRISSGMARKNIAKXIANEL 720

RESULT 8
US-08-677-298-2
; Sequence 2, Application US/08677298
; Patent No. 5863729
; GENERAL INFORMATION:
; APPLICANT: Pimlico-Worms, Helen
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TC4K-1
; TITLE OF INVENTION: KINASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,298
; FILING DATE: 09-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Caruthers, Jennie M.
; REGISTRATION NUMBER: 34,464
; REFERENCE/DOCKET NUMBER: 9-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-677-298-2

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Query Match 22.0% Score 768.5; DB 2; Length 729;
Best Local Similarity 30.1%; Pred. No. 7,4e-49;
Matches 217; Conservative 111; Mismatches 256; Indels 137; Gaps 19;

QY 10 AQHAYGPEYRLKTLGKQGLVGVHCVTQKVAIKYNNREKLSSEVLMKVEREIAI 69
DB 47 ADEQPHIGNYRLTKIGKGFNFAKYLARHIIITGREVAIKIIDKQINPSTQKLFREYRI 106
QY 70 LKLIHPHYKLADHYENKKYLYLVLEHVSGLSDYVKKGRLLPTEKREKFRQIISAL 129
DB 107 MKLHPHYKLVKFEVLETEKTLTYLMEYASGGEVFDVLAQRKMEKAKSKFRQIVANV 166
QY 130 DFCHSHSICHRDLKEKNLIDKNNIRIADFGMASLQVDSLLETSCSPHYACEVIRG 189
DB 167 QYCHQKRIYHRDLKXENLLDADNMTKIADFGSNSEFTVGGKLDTFCCSPYABELFQG 226
QY 190 EKYDGRKADVMSGVIYLPALVGAIPDDDNLRQLLEKVGKGVFMFPIPDQCSLLRG 249
DB 227 KKYDGEVDVWMSLGVILYLVSGSLPFDQNLKELREVRVLRGKXAIPEYMTSDCENILKR 286
QY 250 MIEVDARRLTLEHIOKHIVYIGKNEPEEQPIPRKQVIRSLPSLEDDIDPVLDSMHSI 309
DB 287 FLVLPFKRGITLQIMKDRMIAAGHEDEKFPV-----PELISDQKRIDIWGM 338
QY 310 GCFDRNKLLODLSEBNOEKMIYFLILDRKERYPSQED-EDLPPEIDPPRKRVNSP 368
DB 339 GYQGEB---IQDSLKMKYDEITATYLLGRKS---SELDASSSSSNTSLAKVRPSD 392
QY 369 MNRHCKRPERKSEVLSVD-----GSPVPARARL-----EMAHQGR 409
DB 393 LNNSTG-QSPHKKVQSVSSCKQRRYSDHAGPALPSVAYIKKQTSADGDLKEDGIS 451
QY 410 SRSISGASSGLSTPSLSPVTPHPSPRGSPPLPTPKGTPVHTPKESPA----- 457
DB 452 SRKSSGSAVGAGIAPASPLMGASNPKNADIPERKKSST--VPSNTASGQWTRNTYVC 510
QY 458 -----GTPNTPPS-----SPGVGVPMWARRL--NSIKNSFLGSR 491
DB 511 SERTADRHSVIONGENSTIPDQTPVASTHSISAAITPDIRPRGTASTSTHGQPR 570
QY 492 PRRKLOVPTPEMSNLTPSSPELAKS-----WGNFIS-LEKEBQIFVYIKD----- 540
DB 571 -ERRITVNGPPASPSLSHETPLQTSRGSNTLFSKLTSLTSSRVNASQXQENKKA 629
QY 541 KPLSSIKADIVAHFLISLSHSVISQTSFRAEYATGS--PAVQKPKQVFD----- 592
DB 630 KPRS-----LRFWSMKTSSMDPGDWWRRIKRLVDANNDY 666
QY 593 -----ITYEGGEAKEN-----GIYSVFTLLSGSRPRKRVETIQOL 632
DB 667 EQREPLFCVHGDHAENLVQWEMEVCCLPRLSLNGVRKRISSGTAFAKXIAKIANE 726
QY 633 L 633
DB 727 L 727

RESULT 9
US-09-523-849-33
; Sequence 33, Application US/09523849
; Patent No. 6458561
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Magnani, Angela
; APPLICANT: Magnani, Paola
; APPLICANT: Bosetti, Roberta
; APPLICANT: Scacheri, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIM1 KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849

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/ CURRENT FILING DATE: 2000-03-13  
 / NUMBER OF SEQ ID NOS: 39  
 / SOFTWARE: PERL Program  
 / SEQ ID NO 33  
 / LENGTH: 729  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: misc feature  
 / OTHER INFORMATION: Genbank Accession No. 6458561.g3089349  
 US-09-523-849-33

Query Match 22.0%; Score 768.5; DB 4; Length 729;  
 Best Local Similarity 30.1%; Pred. No. 7.4e-49;  
 Matches 217; Conservative 111; Mismatches 256; Indels 137; Gaps 19;

QY 10 AQAAGVARYLETKGQGTGLVKGVCCTCOKVAIKIVNREKLSBYLAKVEREIAI 69  
 DB 47 ADEQGHIGNYRLKLTIGKGFAYKAKARHILGREGVAIKIIDKQLPTSLQILFREVRI 106  
 QY 70 LKLEHPRVXLHDVYENKLYLVLEHVSGBELFDYLKKGRLLTPREARKFPROIISAL 129  
 DB 107 MKLINHPVIXLFEVIEETKTLVIMEXYASGEVFYLVAHGMRKKEAKSKFRQIVSAV 166  
 QY 130 DFCISHSICHRDIPRENILDERKNIRIADFGMASLQVGSILLETSGSPHYACPEYIRG 189  
 DB 167 QYCHQKRIVHRDLAENLLDADWNIKIADFGFNSNERTVGKLDLTFGSPPYAPAPLFGQ 226  
 QY 190 EKYGRKADWVSCGVIIFALLVGLPFDNDLRLQLEKVRGVFHMHPFIIPDCOSLIRG 249  
 DB 227 KKYGPEDVWVSLGVIITLVSGSLPFDGQNLKELRERVLRGKRIFFYMTDCENLLKR 286  
 QY 250 MIEVDAARLTLEHIQKHIVYIGKNEPEPEQIPRKVQIRSLPSLEDIDPDVLDMSHL 309  
 DB 287 FLVNLPIKRGTLKLEIMDRMINAGHEDELKPFVE-----PELDISQKRDIDWGM 338  
 QY 310 GCFRDNKLTODLSEENQEKMTYFLILDRKERYPCED-EDLPNNEIDPREKVDSP 368  
 DB 339 GYSQGE---IQPSLSKMTYDEITATYLLGRKS---SELDASSSSSSNLAKVRSSD 392  
 QY 369 MLNRHKKRPERKSNVLSVTD-----GGSPVPARRAI-----EMAHQGR 409  
 DB 393 LNNSTG-QSPHKKVQRSVSSQOKORVSDHAGPAIPSVAVPKRSQSTADGDLKEDGIS 451  
 QY 410 SRSISGASSGSLSTPSLSRYTPHPSPRGSPLTPKGPVATPKESPA-----457  
 DB 452 SRKSSGSAVGGKGIAPASPMLGMAKNPKADIPRKSSST-VPSNNYASGCMTRNTYVC 510  
 QY 458 -----GTPNTPPS-----SPSVGGVPWRARL--NSIKNSFLGSPR 491  
 DB 511 SERTADRHVITQCKENSTIPDQRTPVASTHSISASATPDRIRFPRTGASRSTFHQGR 570  
 QY 492 FHRRLQVPTPEMSNLTPESSPELAKS-----WFGNFTS-LEKEQIVVLIKD-----540  
 DB 571 -ERRATVNGPPASPSPISHEATPLSQTSSRGSTNLFSKLTSLRSNNVAEODENKEA 629  
 QY 541 KPLSLIKADIHAFLISPLSHSVISQTSFPAEYKATGG--FAVQKPVFVOVD-----592  
 DB 630 KPRS-----LRFWSMKTTSSMDPGDMKEIKVLDANNCDY 666  
 QY 593 -----ITYTGGGAQKN-----GIYVTFLLSGPERRKRVETIQAQ 632  
 DB 667 EQRERFLFCVHGQHAENLVQWEMEWCKLPRLSLNGVRFRKRIISGTSIAFNIAASKIANE 726  
 QY 633 L 633  
 DB 727 L 727

RESULT 10  
 US-09-523-849-32  
 / Sequence 32, Application US/09523849  
 / Patent No. 6458561

/ GENERAL INFORMATION:  
 / APPLICANT: Bandman, Olga  
 / APPLICANT: Molteni, Angela  
 / APPLICANT: Magnaghi, Paola  
 / APPLICANT: Bosotti, Roberta  
 / APPLICANT: Scacheri, Emanuela  
 / APPLICANT: Isacchi, Antonella  
 / APPLICANT: Hodgson, Dave  
 / TITLE OF INVENTION: HUMAN NIM1 KINASE  
 / FILE REFERENCE: PC-0009 US  
 / CURRENT APPLICATION NUMBER: US/09/523,849  
 / CURRENT FILING DATE: 2000-03-13  
 / NUMBER OF SEQ ID NOS: 39  
 / SOFTWARE: PERL Program  
 / SEQ ID NO 32  
 / LENGTH: 793  
 / TYPE: PRT  
 / ORGANISM: Rattus norvegicus  
 / FEATURE:  
 / NAME/KEY: misc feature  
 / OTHER INFORMATION: Genbank Accession No. 6458561.g2052189  
 US-09-523-849-32

Query Match 21.9%; Score 764.5; DB 4; Length 793;  
 Best Local Similarity 32.7%; Pred. No. 1.6e-48;  
 Matches 193; Conservative 94; Mismatches 185; Indels 119; Gaps 14;

QY 15 YGPRLEKTLGKGTGLVKGVCCTCOKVAIKIVNREKLSBYLAKVEREIAI 74  
 DB 56 HIGNRLOITIGKGFAYKAKARHILGREGVAIKIIDKQLPTSLQILFREVRI 115  
 QY 75 HPHVLKHDVYENKLYLVLEHVSGBELFDYLKKGRLLTPREARKFPROIISALDFCHS 134  
 DB 116 HPHVIXLFEVIEETKTLVIMEXYASGEVFYLVAHGMRKKEAKSKFRQIVSAVOYHQ 175  
 QY 135 HSICHRDLKPEENILDERKNIRIADFGMASLQVGSILLETSGSPHYACPEYIRG 194  
 DB 176 KCIYHRDLKPEENILDERKNIRIADFGFNSNERTVGKLDLTFGSPPYAPAPLFGQ 235  
 QY 195 RKADWVSCGVIIFALLVGLPFDNDLRLQLEKVRGVFHMHPFIIPDCOSLIRG 254  
 DB 236 PEVDWVSLGVIITLVSGSLPFDGQNLKELRERVLRGKRIFFYMTDCENLLKLVLN 295  
 QY 255 AARLTLEHIQKHIVYIGKNEPEPEQIPRKVQIRSLPSLEDIDPDVLDMSHLGCFRD 314  
 DB 296 PIKRGSLQIMDRMANGHEEBE-----LKYSEPELDINDAKRIDIVTWGFPARD 347  
 QY 315 RKKLLODLSEENQEKMTYFLILDRK-----341  
 DB 348 E---INDALVSGKYDEVATYILLGRKPEFEGGESLSSGNLQCRSPSSDLNNSTLOSP 404  
 QY 342 -----ERYPSQDEEDLPP-----RNEIDPPKRV-DSFMLNRHGR 376  
 DB 405 AILKTVQRSANQKRRFSDHAGPSIIPPAVGYTKRPQANSVSEQKEWMDOTARRLGST 464  
 QY 377 R-----PERKMEV---LSVTGGSPVPARRAI-----EMAHQGR 411  
 DB 465 TVGSKSEVTASPLVGPDRKKSAGPSNNVYSGSMTTRNTYVCERSTDRYALANGRSS 524  
 QY 412 SISGASGLSTS-----PLSPRYTPHPSPRSP-----LPTPK-GTPVATPKESPA 458  
 DB 525 LTEMASMSWSTGSIYVAGSPARPRHOKMSSTSHPKYTLPTIKDSEAYRP-----G 579  
 QY 459 TNPPTPSGSPVGV-----PWRARL--NSIKNSFLGSPRHRRLQVPTP 502  
 DB 580 TAQRVPAASPASHSISASTPRTPRPGSSSRSTFHGQLRERSAAYSGP 630

RESULT 11  
 US-09-523-849-34  
 / Sequence 34, Application US/09523849  
 / Patent No. 6458561  
 / GENERAL INFORMATION:

```

; APPLICANT: Bandman, Olga
; APPLICANT: Molteni, Angela
; APPLICANT: Magnaghi, Paola
; APPLICANT: Bosotti, Roberta
; APPLICANT: Scacchi, Emanuela
; APPLICANT: Isacchi, Antonella
; APPLICANT: Hodgson, Dave
; TITLE OF INVENTION: HUMAN NIMI KINASE
; FILE REFERENCE: PC-0009 US
; CURRENT APPLICATION NUMBER: US/09/523,849
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 34
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank Accession No. 6458561 95672676
US-09-523-849-34

Query Match      21.4%; Score 749; DB 4; Length 776;
Best Local Similarity 31.5%; Pred. No. 2.3e-47;
Matches 214; Conservative 87; Mismatches 223; Indels 156; Gaps 20;

Cy 4 TGKDGGAQHAQVGPVPLEKTLGKGTGLVGVHCVTCOKVAIKVNEKLSSEVIMKY 63
Db 12 TGTOGQOQKPLRVGFYVERTLGKGNFAVVKLARHRTVKQVAKIKIDKTRLSNLEKI 71
Cy 64 EREIAIKLLEHPIVTLKLDHYENKKYLYLVLEHVSQGLFDYLVKKGRITPEARKFPR 123
Db 72 YREVQLKLNHPHPIITLYQVMEKMDLYITEFARKGEFDYLSNGHSENBAKKF 131
Cy 124 QIISALDFCHSHSICBBDLKRENILDEKKNIRIADFGMAASLOVGSLLTSCGSPHYAC 183
Db 132 QILSAVYCHNHIVHDLKTEMLLDGNMDIKIADFGFNFKPGEPSTWCGSPHYAA 191
Cy 164 PEVIRGKRYGRKADVSCGVLIFALLVGALEPDDNLRQLLEKVKRGVHMHFIPDC 243
Db 192 PEVEGKRYGRKADVSCGVLIFALLVGALEPDDNLRQLLEKVKRGVHMHFIPDC 251
Cy 244 QSLRGNIEDVDAARLTLEHIOKTIWYIGKNEBEP---EOP1PRKVQIRSLPSLEDDP 300
Db 252 ETLIRRLVVDPAKITIQAIRGRHW---QADPTLLQDDPAFMSQGYTSLGDPVNS 306
Cy 301 DVLDSHSLGCFDRKRLQDLSEENQCKMIFELLDR---KERYPSQDEDDLP 355
Db 307 QVAGIMQALGI--DRQRTVESLQNSSYNHFAIYLLERLRHRSRSTQPSRAATPAFARQ 364
Cy 356 -----NEI---DPEKRVDSFM-----LNHRGKRPP----- 378
Db 365 POLRNSLSSLEVGQELPCDFPRLSLCPOQALASVQALIEDCHLSLOLPFPPLD 424
Cy 379 -----ERKSMVELSVTDGSPVPAPARAIEMAHOGGRSRISGASSGLST-----S 423
Db 425 TNCGCVFRHRSISPSLDTAISSEARQGPSLEEGVQEPPLPGSTGRHRTLLAEVSTHFS 484
Cy 424 PLSGPRVTPHSPRPGSLPTPKGPR---VHTPKESPAG---TPNTPSPSPSVG 472
Db 485 PLNPFCTIVSSSAVSP---SEGTSSDSCLPFSSECPAGIGGLATPGLIGTSSP--- 537
Cy 473 VPMARLINSIKNSFLGSPRFRHRLQVTPPEMSN-----LTPESPSP----- 515
Db 538 -----VRLAS---PLIGS-----QSATPVLSQAGLGAIVLPVPGFQGRASDTSLT 582
Cy 516 -----LAKSNFNGNPLSLEKEBQIFVYIKKPLSSIKADIVAHFLSIPLSHYS 566
Db 583 QGLKAFQOQKRNKARTYGFGLNK-----IKGLAROV-C 615
Cy 567 QTSFAEYKATGDAVFQKP 586
Db 616 QSSIRG---SRGGMSTFHTP 632

```

```

RESULT 12
US-08-817-832B-31
; Sequence 31, Application US/08817832B
; Patent No. 6579691
; GENERAL INFORMATION:
; APPLICANT: MANDELKOW, Eckhard, et al.
; TITLE OF INVENTION: No. 6579691el Protein Kinase (NPK-110)
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 S. Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,832B
; FILING DATE: 28-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/04258
; FILING DATE: 30-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94 11 7122.5
; FILING DATE: 28-OCT-1994
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 779 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-817-832B-31

Query Match      21.4%; Score 749; DB 4; Length 779;
Best Local Similarity 32.4%; Pred. No. 2.3e-47;
Matches 192; Conservative 94; Mismatches 186; Indels 120; Gaps 15;

Cy 15 YGPFVLEKTLGKGTGLVGVHCVTCOKVAIKVNEKLSSEVIMKVEBIAIKLIE 74
Db 42 HIGNTRLOKTIKGNPAKVKLARHVTGRBAVAKIKIDKTLQNPISLOKLFREVRIMKILN 101
Cy 75 HPHVTLKLDVYENKKYLYLVLEHVSQGLFDYLVKKGRITPEARKFROITISALDFCHS 134
Db 102 HENIVLFEVIEETEXTLYLVMEYASGGEVFDYLVHGHMKKEKARAKFROIVSAVOYCHQ 161
Cy 135 HSICRDLKPEVLLDEKKNIRIADFGMAASLOVGSLLTSCGSPHYACPEVIRGKRYGR 194
Db 162 KCIIVHDLKAEMLLDADNMTIKIADFGSNERTVANKLDTFGSPHYAPPELFOGAKTIDG 221
Cy 195 RZADWYSGCVILFALLVGALEPDDNLRQLLEK-VKRGVFNHPIIPDCGSLRGMTIEV 253
Db 222 PEVDWWSLGVLITLVSGSLPDDGQNLKELRERSCLRGKRVYFPWSTDCERTLKKLVL 281
Cy 254 DAARLTLEHIOKTIWYIGKNEBEPPOPIRKVQIRSLPSLEDDPDLVDSHSLGCFR 313
Db 282 NPIKRGSLQIKMDKMNWVGHHEEB-----LKPYSPELIDNDAKRIDIVTMGPAR 333
Cy 314 DENKLLDLSSEENQCKMIFELLDR-----RNEIDPPRKV-DSPVLMNRGK 375
Db 334 DE---INDALVSOXKDEVATYIILGRKPRPEEGSGSLSSGNLCQSRSPSSDIANKSTIQS 390
Cy 342 -----ERYPSQDEDDLP-----RNEIDPPRKV-DSPVLMNRGK 375
Db 391 PAHLKVORTISANOKORRFSDHAGPSIDPAVSYTRPOANSYSEBQKEBWDKTAARRIGS 450
Cy 376 RR-----PERKSMVEV---LSVTGSGSPVPARAI-----EMAHGGRS 410

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Db      451 TTGSKSEVTASPLVGDRKSSAGPSNNVYSGSMTTRNTYTCERSTDRYALLOGRS 510
Qy      411 RSISGSSGSLTS-----PLSPRVTPHPSPRSP-----LPTPK-GTPVHTPKESPA 457
Db      511 SLNEMSSMSSTGTSVYASAGPAPRHQKSMSTSGHPIKVTLPFIKDSSEAYRP----- 565
Qy      458 GTNPTPTPSSPSVGV---PWARL---NSINKSLGSRFRRLQLQVPTP 502
Db      566 GTAQRVAPASPSAHISASTPDRTPRPPRGSSSRSTHGQLRERRSAAYSGP 617

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## RESULT 13

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; Sequence 5, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-799-875-5

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## Query Match

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; Best Local Similarity 21.2%; Score 740; DB 4; Length 1203;
; Matches 189; Conservative 90; Mismatches 162; Indels 112; Gaps 16;

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Qy      16 VGPRLKRTLGKGTGLVYGVHCVCQKVAIKIVREKLSSEVLMKVEEELIKLIEH 75
Db      5 IGYEIDRTTGKGFVAVKRAHILVYAKVAIKIIDTQDEENLKIFREVIIMKMLCH 64
Qy      76 PHLVLDVYENKCYLVLEHVSQGLPDYLVKGRILTPKARKFFRQIISALDCHSH 135
Db      65 PHIRLVQVWETEMITLVTEVYASGGEIFDLVHAGMAEKARKEKQIVTAVYFCGR 124
Qy      136 SICGRDLKPERYLLDEKNRIADFGMASIQVDSLIETSCGSPHYACPEVIRGEKYDR 195
Db      125 NIVHRDKAENLLDANLNIKIADFGFSNLFPGQILKTWCSPPAAPLFEKGKEYDGP 184
Qy      196 KADVWSGVILFALLVGLPDDDNLRQLLEKVRGVFHPHPIPPDCOSILRGMEVDA 255
Db      185 KVDVWSIGVYIVYVCGALPPDSTLQNLARVLSGKFRIPFMSIECHELIHMLVLP 244
Qy      256 ARRLLEHIOGHIMYIGKNEPEPEQPIPRKVOIRSLPSLEIDIDPVLYDSHSLGCFRDR 315
Db      245 NKRLSMEOICGKMMKLGADAPNFDRLIAECQOKERROYD PLINEDVILAMEDMG- -DX 302
Qy      316 NKILQ-----DILS-----EENOEKMIYELLDR- 340
Db      303 EQTLQAEQAGTANMISVPOVLINPENQIVPEPDTLMLDSEGEPSPEALVYLSMRKH 362
Qy      341 -----KERYSQED--EDLPRNEIDP--PRKRVDS-----PMLNHGKRPERKS 382
Db      363 TVGVADRTEVMEVLDKLLPGFPGVAPQAPFLQVAPVNVFMHNLIPQNIQPTGOLEYKE 422
Qy      383 MEV-----LSVTGDSVVPARRALEMAHQGRSSISGASSGSTSPSLSPRTYPPSPR 437
Db      423 QSLQPTLQILNMGFL-GRRA-----SDGGANIQIHAQQLK-----RPR 463

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```

Qy      438 G-SPLPT-----PKGTPEVHTPKESPACTP-----NPT-----PPS 466
Db      464 GPSPPLMTTAVPAPVATVY--DEBSSDGEPPQEAQRYLANRSKRHTLAMNPFAELPPDL 521
Qy      467 SPVSGVPPWARRL 479
Db      522 QRLGQQQPFRRSRV 534

```

## RESULT 14

```

; Sequence 40, Application US/0855706C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Beri, Rajinder K.
; APPLICANT: Carling, David
; APPLICANT: Forde, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PH37588/UST
; CURRENT APPLICATION NUMBER: US/08/557,066C
; PRIOR FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Rat
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1747)
; OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -
; OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
; OTHER INFORMATION: nucleotide 1765
; US-08-557-006C-40

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## Query Match

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; Best Local Similarity 20.9%; Score 729.5; DB 3; Length 552;
; Matches 197; Conservative 103; Mismatches 217; Indels 143; Gaps 22;

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Qy      16 VGPRLKRTLGKGTGLVYGVHCVCQKVAIKIVREKLSSEVLMKVEEELIKLIEH 74
Db      13 IGHVYLGTTGVGTFGRKYGEGHQLTGHKVAVKILNQKIRSLDVVGKIRKELQNLKLR 72
Qy      75 PHLVLDVYENKCYLVLEHVSQGLPDYLVKGRILTPKARKFFRQIISALDCHSH 134
Db      73 HPHIILYQVISTPDPFMWMEYVSGGELPFYICGHRVVEVARRLFOQLISAVDYCHR 132
Qy      135 HSICGRDLKPERYLLDEKNRIADFGMASIQVDSLIETSCGSPHYACPEVIRGEKYDR 194
Db      133 HNVVHRDLKPERYLLDQMNAKIADFGISNMKSDGEELRTSCGSPNYAAPEVISGRYAG 192
Qy      195 KADVWSGVILFALLVGLPDDDNLRQLLEKVRGVFHPHPIPPDCOSILRGMEVDA 254
Db      193 PEVDVWSGVILYALLCGLPDDSHVFTLPKIRGVGYFIPTILNLSIATILMHMLQVD 252
Qy      255 AARRLLEHIOGHIMYIGKNEPEPEQPIPRKVOIRSLPSLEIDIDPVLYDSHSLGCFRDR 315
Db      253 PLKRTIIDIREFHEMF-----KQDLPSYL-----FPEDPSYDANVIDEAVKEVCEK 299
Qy      309 LGCFPRDKMLQDILS--EENOEKMIYELLDRKERYPSQED-----DLPRNEIDPARK 363
Db      300 FEC--TSEVWNLSYSGPQDQVAVYALIDNR-RIMNQSEFYTLASSPFTG----- 349
Qy      364 RVDSPMLNRHGKRPERKSMELSVTGGSPVPPARRALEMAHQGRSSISGASSGSTS 423
Db      350 -----SFMQ-----DVMNH----- 358

```

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QY 424 PLSPRTVPHSPRGSPL--PTPKGTVPHTPKSPACTVPTPPSSPSGVCVPMRRLNS 481
Db 359 --IPGKAPRPE--MPPPLADSPFA-----RCPDLALNTTPKSLAVKAKMHLGINS 408
QY 482 IKNSFLGSPRPHRRKLQVPTPEENSNL---TPSSPELAKKSMFGNFIILEKEOIFVY 537
Db 409 OSKPYDIAEVYAMKQLDFEMKVNAYHLRVARKNPVT-----GNVYVMSL--QLYLY 460
QY 538 IKKPELSSIKADIVHAALSLPSLSHSVTSQTSFRAEYKATGPAVPOKPVKFOVDITYIE 597
Db 461 -----DKRSYLLDFKSLIDDEVYEQSGSSTPQRSASAGLHRP--RSSVDSSTAE 508
QY 598 GGAOKENGIVYVFTLLSGPSRRFRKVEITIOQLSTDPDPAOHLSPDTN--CENMT 656
Db 509 NHS-----LSG-----SLTGSITGSLTSSASPRLGSHTMDFEMCASLIT 548

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RESULT 15
US-08-557-006C-43
; Sequence 43, Application US/08557006C
; Patent No. 6258547
; GENERAL INFORMATION:
; APPLICANT: Bert, Rajindar K.
; APPLICANT: Carling, David
; APPLICANT: Forster, Robert A.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
; FILE REFERENCE: NGAP/PHN37588/UST
; CURRENT APPLICATION NUMBER: US/08/557, 006C
; PRIOR FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: PCT/GB94/01093
; PRIOR FILING DATE: 1994-05-20
; PRIOR APPLICATION NUMBER: GB 9310489.1
; PRIOR FILING DATE: 1993-05-21
; PRIOR APPLICATION NUMBER: GB 9318010.7
; PRIOR FILING DATE: 1993-08-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Yeast
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(633)
; OTHER INFORMATION: Yeast SNF1 polypeptide
US-08-557-006C-43

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Query Match          20.64; Score 720.5; DB 3; Length 633;
Best Local Similarity 33.64; Pred. No. 2.3e-45;
Matches 158; Conservative 109; Mismatches 152; Indels 51; Gaps 11;

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QY 15 YVGPYLEKTLGKQGTGLVKGVHCVTCQKVAIKIVNREKLSSEVLM-KYEREIALIKLI 73
Db 51 HIGVQIVKTLGGSGFGKVTGLAVHTTGQKVALKIKKVIKAKSDMQGRIBREISYLRLL 110
QY 74 EHHVTLKLVHVENKTLIVLVLEHVSGLLFDVLYKKGRITPKKARKPRQIISALDPCH 133
Db 111 RHPHIIILYLVIVISKOEIINWIEY-AGNELFDYIVQDKMSQEQARRFQOIISAVEYCH 169
QY 134 SHSICERDLKPEMLLDKKNIRIADFGMASLQVGSILLETSGSPHYACPEVIREGEYD 193
Db 170 RHKIVRHDLKPEMLLDKKNIRIADFGMASLQVGSILLETSGSPHYACPEVIREGEYD 229
QY 194 GRKADVWSCGVIIIPALIVGALPPDDDNLRQLLEKVRGVFHMHPFIIPDCQSLRGMIY 253
Db 230 GPEVDVWSCGVIIIPALIVGALPPDDDNLRQLLEKVRGVFHMHPFIIPDCQSLRGMIY 289
QY 254 DAARRLTLEHIOKHIWYIG-----KNEPEPEQPIPRKVOIRSLPSLEDIDPDVL 303
Db 290 NPLNRSIHETIMQDDMKVLPPEYLLPDLKPRPEEENENNDKSGSSPDNDEIDNLY 349
QY 304 DSMHSIAGCFPRNKLLODLISEE---NOEKMIYFLLIDRKERYPSQF---DEDLPP 354

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Db 350 NILSTMGV-EKDEIYESLESSEDTPAFNEIRDAYMLIKENKSLIKOMKANKSVSDELD 408
QY 355 RNEIDP-----RRYDSFMLNHRKRPRPKSMKMEVLSYTDGSSVPAPARALEMA 404
Db 409 FLSQSPPTFOQSKSHOKSCVDHETAKQHARRM-----ASAITQOQRTYHQS 454
QY 405 QHGQRSRISGASGLSTSPSSPRV-TPHSPRGSPLPTPKGTVPHTPK 453
Db 455 PMDQYKE---EDSTVSLPTSLPQIRANMLAQSSPAAS-KISPLVTKK 500

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Search completed: July 29, 2004, 10:27:22  
Job time : 22 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 10:25:56 ; Search time 50 Seconds

(without alignments)  
4190.804 Million cell updates/sec

Title: US-10-054-579-2

Perfect score: 3497

Sequence: 1 MSTGKGAGAGHAYGVYR.....TNCMEMTGRSLKCGIIPKS 668

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3497	100.0	668	US-10-054-579-2	Sequence 2, Appli
2	3497	100.0	668	US-10-195-072-2	Sequence 2, Appli
3	3497	100.0	668	US-10-195-071-2	Sequence 2, Appli
4	3423	97.9	664	US-10-362-892-18	Sequence 18, Appli
5	3423	97.9	664	US-10-288-798-18	Sequence 18, Appli
6	3380	96.7	674	US-10-283-247-2	Sequence 2, Appli
7	3374	96.5	674	US-09-842-582-2	Sequence 2, Appli
8	3374	96.5	674	US-10-283-247-7	Sequence 7, Appli
9	3374	96.5	674	US-10-283-247-8	Sequence 8, Appli
10	3200	91.5	688	US-10-425-114-54467	Sequence 54467, A
11	3188	91.2	608	US-10-054-579-4	Sequence 4, Appli
12	3065	87.6	614	US-10-283-247-9	Sequence 9, Appli
13	3065	87.6	614	US-10-283-247-10	Sequence 10, Appli
14	3050	87.2	636	US-10-283-247-5	Sequence 5, Appli
15	3028	86.6	585	US-10-195-072-4	Sequence 4, Appli

16	3028	86.6	585	14	US-10-195-071-4	Sequence 4, Appli
17	3015	86.2	603	14	US-10-195-072-17	Sequence 17, Appli
18	3015	86.2	603	14	US-10-195-071-17	Sequence 17, Appli
19	2799	80.0	778	12	US-10-423-543-11	Sequence 11, Appli
20	2799	80.0	778	14	US-10-354-358-92	Sequence 92, Appli
21	2799	80.0	778	14	US-10-116-326-2	Sequence 2, Appli
22	2785.5	79.7	703	14	US-10-311-034-17	Sequence 1, Appli
23	2545.5	72.8	703	14	US-10-116-326-6	Sequence 6, Appli
24	2386.5	68.2	762	12	US-10-116-326-4	Sequence 4, Appli
25	1537.5	44.0	506	12	US-10-425-114-54189	Sequence 54189, A
26	1275.5	36.5	301	12	US-10-276-774-1422	Sequence 1422, Ap
27	871.5	24.9	1349	16	US-10-618-581-16	Sequence 16, Appl
28	796.5	22.8	745	12	US-10-260-708-79	Sequence 79, Appl
29	796.5	22.8	745	12	US-10-260-708-79	Sequence 36, Appl
30	796.5	22.8	745	14	US-10-195-101-36	Sequence 36, Appl
31	794.5	22.7	691	9	US-10-161-565-24	Sequence 24, Appl
32	794.5	22.7	724	9	US-09-919-585-6	Sequence 6, Appli
33	793.5	22.7	724	15	US-09-919-585-9	Sequence 9, Appli
34	793.5	22.7	724	15	US-10-274-194-2	Sequence 2, Appli
35	793.5	22.7	1462	16	US-10-618-581-15	Sequence 15, Appl
36	792.5	22.7	722	15	US-10-274-194-4	Sequence 4, Appli
37	792.5	22.7	722	16	US-10-760-407-4	Sequence 4, Appli
38	790.5	22.6	514	12	US-10-183-687-248	Sequence 248, App
39	790.5	22.6	722	8	US-08-817-8328-32	Sequence 32, Appl
40	790.5	22.6	722	12	US-10-440-435-32	Sequence 32, Appl
41	790	22.6	1518	9	US-09-801-368-152	Sequence 152, App
42	790	22.6	1518	15	US-10-369-993-22243	Sequence 22243, A
43	790	22.6	1518	16	US-10-618-581-11	Sequence 11, Appl
44	788	22.5	769	12	US-10-363-616-403	Sequence 403, App
45	787	22.5	545	12	US-10-425-114-62429	Sequence 62429, A

## ALIGNMENTS

RESULT 1									
US-10-054-579-2									
; Sequence 2, Application US/10054579									
; Publication No. US20020137913A1									
; GENERAL INFORMATION:									
; APPLICANT: Turner, C. Alexander Jr.									
; APPLICANT: Mathur, Brian									
; TITLE OF INVENTION: No. US20020137913A1 Human Kinases and Polynucleotides Encoding									
; FILE REFERENCE: LEX-0300-USA									
; CURRENT APPLICATION NUMBER: US/10/054,579									
; CURRENT FILING DATE: 2002-01-22									
; PRIOR APPLICATION NUMBER: US 60/263,378									
; PRIOR FILING DATE: 2001-01-23									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 668									
; TYPE: PRT									
; ORGANISM: homo sapiens									
US-10-054-579-2									
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Best Local Similarity 100.0%; Score 3497; DB 13; Length 668;									
Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MSTGKGAGAGHAYGVYRLEKTKGKQGTGLVKGVCVTCOKAIVREKISBVL	60						
DB	1	MSTGKGAGAGHAYGVYRLEKTKGKQGTGLVKGVCVTCOKAIVREKISBVL	60						
QY	61	MVEREIAIILKIEHPHLKLDVYENKKYLYLVLEHSGSLFDPYLVKGRITPEARK	120						
DB	61	MVEREIAIILKIEHPHLKLDVYENKKYLYLVLEHSGSLFDPYLVKGRITPEARK	120						
QY	121	FRQIISALDFCHSHSICHRDIPENLLDKENNRIRDFGMAISQVDSLETSCGSPH	180						
DB	121	FRQIISALDFCHSHSICHRDIPENLLDKENNRIRDFGMAISQVDSLETSCGSPH	180						
QY	181	YACPEVINGEKXDKKADVWSCGVLFPALVGLPFDNDNRQLLEKVRGVFHPHPFLP	240						



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Db      181 YACEVIRGEKXDKRKADWVSCGVIPLFALLVGALPFDDNLRQLLEKVRGVFHMHPFIIP 240
Qy      241 PDCOSLRGMIEVDAAARLTLEHIQKHIWYIGKNBEPEOPIPRKVOISLSLEIDIP 300
Db      241 PDCOSLRGMIEVDAAARLTLEHIQKHIWYIGKNBEPEOPIPRKVOISLSLEIDIP 300
Qy      301 DVLDSMSLGCFFRDNKLLDPLSEENOEKMIYFLLDKRERYPSQEDDLPPRNEIDP 360
Db      301 DVLDSMSLGCFFRDNKLLDPLSEENOEKMIYFLLDKRERYPSQEDDLPPRNEIDP 360
Qy      361 PRKRVDSFMLNRHGRKRRPERKSMELVSTDGSPVPARRAIEMAHQGRSRISGASGL 420
Db      361 PRKRVDSFMLNRHGRKRRPERKSMELVSTDGSPVPARRAIEMAHQGRSRISGASGL 420
Qy      421 STSPLSSPRVTPHSPSPGSPPLPTPKGTPVHTPKESPAGTNPPTPSSPSVGGVPMWRRLN 480
Db      421 STSPLSSPRVTPHSPSPGSPPLPTPKGTPVHTPKESPAGTNPPTPSSPSVGGVPMWRRLN 480
Qy      481 SIKNSFLGSPFRHRRKLOVPTPEMSNLTPESSPELAKKSMFGNFIISLEKEEQIFVVIKD 540
Db      481 SIKNSFLGSPFRHRRKLOVPTPEMSNLTPESSPELAKKSMFGNFIISLEKEEQIFVVIKD 540
Qy      541 KPSSIRKADIVHAFLSLPSLSHSHVTSQTSFRAEYKATGPAVFOKPVKFQVDITYEGGE 600
Db      541 KPSSIRKADIVHAFLSLPSLSHSHVTSQTSFRAEYKATGPAVFOKPVKFQVDITYEGGE 600
Qy      601 AQKNGIYSVTFTLLSGSPRRFRKRVETIQAOILSTHDPRAOHLSDTTNOMEMTGRLS 660
Db      601 AQKNGIYSVTFTLLSGSPRRFRKRVETIQAOILSTHDPRAOHLSDTTNOMEMTGRLS 660
Qy      661 KCGIIPKS 668
Db      661 KCGIIPKS 668

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US-10-195-072-2
; Sequence 2, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195, 072
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-072-2

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Query Match      100.0%; Score 3497; DB 14; Length 668;
Best Local Similarity 100.0%; Pred. No. 8,6e-218;
Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MTSTGKDGAGHAQYVGPYRLEKTLGKQGTGLVGLGVHCVTCQKVAIKIVNREKLSSEVL 60
Db      1 MTSTGKDGAGHAQYVGPYRLEKTLGKQGTGLVGLGVHCVTCQKVAIKIVNREKLSSEVL 60
Qy      61 MKVEREIAIILKLIIEHPVHLKLADYVENKRYLYLVLEHVSQGEPLDYLVKGRILTPKEARK 120
Db      61 MKVEREIAIILKLIIEHPVHLKLADYVENKRYLYLVLEHVSQGEPLDYLVKGRILTPKEARK 120
Qy      121 FFRQIISALDPCGSHSICHRDLKPEENLLDEKNNIRIADFGMASIQVDSILFTSCGSPH 180
Db      121 FFRQIISALDPCGSHSICHRDLKPEENLLDEKNNIRIADFGMASIQVDSILFTSCGSPH 180
Qy      181 YACEVIRGEKXDKRKADWVSCGVIPLFALLVGALPFDDNLRQLLEKVRGVFHMHPFIIP 240

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Db      181 YACEVIRGEKXDKRKADWVSCGVIPLFALLVGALPFDDNLRQLLEKVRGVFHMHPFIIP 240
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Db      241 PDCOSLRGMIEVDAAARLTLEHIQKHIWYIGKNBEPEOPIPRKVOISLSLEIDIP 300
Qy      301 DVLDSMSLGCFFRDNKLLDPLSEENOEKMIYFLLDKRERYPSQEDDLPPRNEIDP 360
Db      301 DVLDSMSLGCFFRDNKLLDPLSEENOEKMIYFLLDKRERYPSQEDDLPPRNEIDP 360
Qy      361 PRKRVDSFMLNRHGRKRRPERKSMELVSTDGSPVPARRAIEMAHQGRSRISGASGL 420
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Qy      421 STSPLSSPRVTPHSPSPGSPPLPTPKGTPVHTPKESPAGTNPPTPSSPSVGGVPMWRRLN 480
Db      421 STSPLSSPRVTPHSPSPGSPPLPTPKGTPVHTPKESPAGTNPPTPSSPSVGGVPMWRRLN 480
Qy      481 SIKNSFLGSPFRHRRKLOVPTPEMSNLTPESSPELAKKSMFGNFIISLEKEEQIFVVIKD 540
Db      481 SIKNSFLGSPFRHRRKLOVPTPEMSNLTPESSPELAKKSMFGNFIISLEKEEQIFVVIKD 540
Qy      541 KPSSIRKADIVHAFLSLPSLSHSHVTSQTSFRAEYKATGPAVFOKPVKFQVDITYEGGE 600
Db      541 KPSSIRKADIVHAFLSLPSLSHSHVTSQTSFRAEYKATGPAVFOKPVKFQVDITYEGGE 600
Qy      601 AQKNGIYSVTFTLLSGSPRRFRKRVETIQAOILSTHDPRAOHLSDTTNOMEMTGRLS 660
Db      601 AQKNGIYSVTFTLLSGSPRRFRKRVETIQAOILSTHDPRAOHLSDTTNOMEMTGRLS 660
Qy      661 KCGIIPKS 668
Db      661 KCGIIPKS 668

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; Publication No. US20030096271A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C1
; CURRENT APPLICATION NUMBER: US/10/195, 071
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-071-2

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Query Match      100.0%; Score 3497; DB 14; Length 668;
Best Local Similarity 100.0%; Pred. No. 8,6e-218;
Matches 668; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MTSTGKDGAGHAQYVGPYRLEKTLGKQGTGLVGLGVHCVTCQKVAIKIVNREKLSSEVL 60
Db      1 MTSTGKDGAGHAQYVGPYRLEKTLGKQGTGLVGLGVHCVTCQKVAIKIVNREKLSSEVL 60
Qy      61 MKVEREIAIILKLIIEHPVHLKLADYVENKRYLYLVLEHVSQGEPLDYLVKGRILTPKEARK 120
Db      61 MKVEREIAIILKLIIEHPVHLKLADYVENKRYLYLVLEHVSQGEPLDYLVKGRILTPKEARK 120
Qy      121 FFRQIISALDPCGSHSICHRDLKPEENLLDEKNNIRIADFGMASIQVDSILFTSCGSPH 180
Db      121 FFRQIISALDPCGSHSICHRDLKPEENLLDEKNNIRIADFGMASIQVDSILFTSCGSPH 180
Qy      181 YACEVIRGEKXDKRKADWVSCGVIPLFALLVGALPFDDNLRQLLEKVRGVFHMHPFIIP 240

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Db 181 YACEVIRGERKTDORAKDWSGVITLALVGLALPDDDLRLQLEKRVGVHMHFIP 240
QY 241 PDCQSLRGMIIEVDAARLTLEHIQKAIWIYIGKNEPEEPOP1PRKQVIRSLPSLEDIDP 300
Db 241 PDCQSLRGMIIEVDAARLTLEHIQKAIWIYIGKNEPEEPOP1PRKQVIRSLPSLEDIDP 300
QY 301 DVLDMSHSLGCFRPNKLLQDLSEENQKMIYFLLDKKRYPSQEDDLPRNEIDP 360
Db 301 DVLDMSHSLGCFRPNKLLQDLSEENQKMIYFLLDKKRYPSQEDDLPRNEIDP 360
QY 361 PRKVDSPMLNRHGRKRRPERKSMVELSVTDGSGFVPARRA1EMA0H0GSRIS1SGASGL 420
Db 361 PRKVDSPMLNRHGRKRRPERKSMVELSVTDGSGFVPARRA1EMA0H0GSRIS1SGASGL 420
QY 421 STSLSPRYTPPHSPGSP1PTPKGTPTVTPKESPAGTNP1PPSPSPVGVPMWRLN 480
Db 421 STSLSPRYTPPHSPGSP1PTPKGTPTVTPKESPAGTNP1PPSPSPVGVPMWRLN 480
QY 481 SIKSFFGSPFRHKKLVPTPEEMSNLTPESSPELAKSGFISLEKEEQIFVYIKD 540
Db 481 SIKSFFGSPFRHKKLVPTPEEMSNLTPESSPELAKSGFISLEKEEQIFVYIKD 540
QY 541 KPLSSIRADIYHAFSLIPSLSHSVISQTSFPAEYKATGPAVFOKPYKFOVDITTYEGGE 600
Db 541 KPLSSIRADIYHAFSLIPSLSHSVISQTSFPAEYKATGPAVFOKPYKFOVDITTYEGGE 600
QY 601 AQKNGIYSVTFTLLSGPSRRFKRVETIQAOQLSTHDPAAOHLSDTTNCMEMTGRSL 660
Db 601 AQKNGIYSVTFTLLSGPSRRFKRVETIQAOQLSTHDPAAOHLSDTTNCMEMTGRSL 660
QY 661 KCGIIPKS 668
Db 661 KCGIIPKS 668

RESULT 4
US-10-362-892-18
; Sequence 18, Application US/10362892
; Publication No. US20040038881A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga
; APPLICANT: NGUYEN, Daniel B.; WALIA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Montique G.
; APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal
; APPLICANT: DING, Li; PATTERSON, Chandra S.
; APPLICANT: YUE, Henry; BAUGHN, Mariah R.
; APPLICANT: TRIBOULEY, Catherine M.; THORNTON, Michael B.
; APPLICANT: ELLIOTT, Vicki S.; LU, Yan
; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
; APPLICANT: LAL, Preeti G.; RAMKUMAR, Jayalaxmi
; APPLICANT: WARREN, Bridget A.; KEARNEY, Liam
; APPLICANT: POLICKY, Jennifer L.; THANGAVELU, Kavitha
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PF-0209 USN
; CURRENT APPLICATION NUMBER: US/10/362,892
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29

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; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20040038881A1 4022651CD1
US-10-362-892-18

Query Match          97.9% Score 3423; DB 12; Length 664;
Best Local Similarity 100.0%; Pred. No. 5.2e-213;
Matches 654; Conservative 0; Mismatches 0; Gaps 0;

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Db 11 YVGPRYLEKTLGKGTGLVKLGVCVTCQKVAIKIYNEKLSSEVLMKVEREIALIKLIE 70

QY 75 HPHVLTLDHYVNNKTYLYLLEHVGGBLFDVLYKKGLTTPKAKFPROIISALDFCHS 134
Db 71 HPHVLTLDHYVNNKTYLYLLEHVGGBLFDVLYKKGLTTPKAKFPROIISALDFCHS 130

QY 135 HSICRDLKPEMLLDEKKNIRIADFGMASLQVGDLSLETSGSPHYACPEVIRGEKYDG 194
Db 131 HSI CRDLKPEMLLDEKKNIRIADFGMASLQVGDLSLETSGSHYACPEVIRGEKYDG 190

QY 195 RKADWMSGVIIIPALIVGALPDDDNLRQLEKXKRGVFMHMF1PPDCQSLRGKIEVD 254
Db 191 RKADWMSGVIIIPALIVGALPDDDNLRQLEKXKRGVFMHMF1PPDCQSLRGKIEVD 250

QY 255 AARBLTLEHIQKHIWIYIGKNEPEEPOP1PRKQVIRSLPSLEDIDPVDVDSMHSJGCFRD 314
Db 251 AARBLTLEHIQKHIWIYIGKNEPEEPOP1PRKQVIRSLPSLEDIDPVDVDSMHSJGCFRD 310

QY 315 RNKLLQDLSEENQKMIYFLLDKKERYPSQEDDLPRNEIDP1PRKRVDSFMLNRHG 374
Db 311 RNKLLQDLSEENQKMIYFLLDKKERYPSQEDDLPRNEIDP1PRKRVDSFMLNRHG 370

QY 375 KRRPEKSMENVLSYDGGSPVPARRA1EMA0G0SRIS1SGASGLSTSPSPRYTPHP 434
Db 371 KRRPEKSMENVLSYDGGSPVPARRA1EMA0G0SRIS1SGASGLSTSPSPRYTPHP 430

QY 435 SPRGSP1PTPKGTPTVTPKESPAGTNP1PPSPSPVGVPMWRLN1KNSFLGSPFRHR 494
Db 431 SPRGSP1PTPKGTPTVTPKESPAGTNP1PPSPSPVGVPMWRLN1KNSFLGSPFRHR 490

QY 495 RKIQVTPPEMGNLTPESSPELAKSGFNF1SLEKEEQIFVYIDKPLSIRKADIVAHF 554
Db 491 RKIQVTPPEMGNLTPESSPELAKSGFNF1SLEKEEQIFVYIDKPLSIRKADIVAHF 550

QY 555 LSTPSLSHVSIVISQTSFPAEYKATGPAVFOKPYKFOVDITTYEGGAQKENGISYVFTL 614
Db 551 LSTPSLSHVSIVISQTSFPAEYKATGPAVFOKPYKFOVDITTYEGGAQKENGISYVFTL 610

QY 615 LSGPSRRFKRVVETIQAOQLSTHDPAAOHLSDTTNCMEMTGRSLKCGIIPKS 668
Db 611 LSGPSRRFKRVVETIQAOQLSTHDPAAOHLSDTTNCMEMTGRSLKCGIIPKS 664

RESULT 5
US-10-288-798-18
; Sequence 18, Application US/10288798
; Publication No. US20030207299A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B.
; APPLICANT: WALIA, Narinder K.; HAFALIA, April J.A.;
; APPLICANT: YAO, Montique G.; GANDHI, Ameena R.;
; APPLICANT: GURURAJAN, Rajagopal; DING, Li;

```

```

; APPLICANT: PATTERSON, Chandra; YUE, Henry;
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael; ELIOT, Vicki S.;
; APPLICANT: LU, Yan; ISON, Craig H.;
; APPLICANT: AU-YOUNG, Janice; TRANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
; APPLICANT: LU, Dyung Aina M.; LAU, Preeti G.;
; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
; APPLICANT: THANGAVEILU, Kavitha; BURFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0209 USA
; CURRENT APPLICATION NUMBER: US/10/288,798
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/240,542
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/238,389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/236,499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/234,902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/231,357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/229,873
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 18
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030207299A1 4022651CD1
US-10-288-798-18

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Query Match          97.9%; Score 3423; DB 15; Length 664;
Best Local Similarity 100.0%; Pred. No. 5,2e-213;
Matches 654; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 YVGPRLKLTGKQGTGLVKGVCVTCQKAIKIIVNREKLSSEVLMKVEREIAILKLE 74
DB 11 YVGPRLKLTGKQGTGLVKGVCVTCQKAIKIIVNREKLSSEVLMKVEREIAILKLE 70
QY 75 HPHVLKLDVYENKKYLYLVLEHVSQGLFPDYLVKGRILPFXEARKKFFROIISALDFCHS 134
DB 71 HPHVLKLDVYENKKYLYLVLEHVSQGLFPDYLVKGRILPFXEARKKFFROIISALDFCHS 130
QY 135 HSICHRDLKPEPNLLDEKNRIADFGMASIQVDSLSLETSCGSPHYACBEVIRGEKYDG 194
DB 131 HSICHRDLKPEPNLLDEKNRIADFGMASIQVDSLSLETSCGSPHYACBEVIRGEKYDG 190
QY 195 RKADVSGCVILFALLVGALEPDDDNRLRLLEKXGQVFMHPHPIPDCCOSILRGMEYVD 254
DB 191 RKADVSGCVILFALLVGALEPDDDNRLRLLEKXGQVFMHPHPIPDCCOSILRGMEYVD 250
QY 255 AARLTLLEHIGKIWIYIGKNEPEPEPIPRKVOIRSLPSLEIDIPDVLDSMHSIGCFRD 314
DB 251 AARLTLLEHIGKIWIYIGKNEPEPEPIPRKVOIRSLPSLEIDIPDVLDSMHSIGCFRD 310
QY 315 RNKLLODLSSEENOEKVIYFLLLDRKERYPSQDEDELPPNNEIDPPRKVDSYMLNRHG 374
DB 311 RNKLLODLSSEENOEKVIYFLLLDRKERYPSQDEDELPPNNEIDPPRKVDSYMLNRHG 370
QY 375 KRRPKSKMEVLYSTVDGSPVPARAIEMAHGQRSSISGASGSLSTSPLSRPVTPAP 434
DB 371 KRRPKSKMEVLYSTVDGSPVPARAIEMAHGQRSSISGASGSLSTSPLSRPVTPAP 430

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QY 435 SPRGSPPLTPKGTVPHTPKESPACTNPNTPPSSPSVGVGVPWRARLNISIKNSFLGSPRRH 494
DB 431 SPRGSPPLTPKGTVPHTPKESPACTNPNTPPSSPSVGVGVPWRARLNISIKNSFLGSPRRH 490
QY 495 RKLQVPTPEEMSNLTPSSPELAKSMFGNLSLEKEQIIVVLDKRLSSIKADIYAF 554
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QY 555 LSIPLSHSVLSQTSFRAEYATGGPAVFOKPVKFOVDITTEGGAQKENGIVSVFTL 614
DB 551 LSIPLSHSVLSQTSFRAEYATGGPAVFOKPVKFOVDITTEGGAQKENGIVSVFTL 610
QY 615 LSGSRPRPRVETIQAOILLSTHDPRAOHISDTTCNEMMTGRLSKGIIIPKS 668
DB 611 LSGSRPRPRVETIQAOILLSTHDPRAOHISDTTCNEMMTGRLSKGIIIPKS 664

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## RESULT 6

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US-10-283-247-2
; Sequence 2; Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLOU1304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-247-2

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Query Match          96.7%; Score 3380; DB 14; Length 674;
Best Local Similarity 99.8%; Pred. No. 3,2e-210;
Matches 646; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSKDGGAQHAQVYGYRLBKLTGKQGTGLVKGVCVTCQKAIKIIVNREKLSSEVL 60
DB 1 MTSKDGGAQHAQVYGYRLBKLTGKQGTGLVKGVCVTCQKAIKIIVNREKLSSEVL 60
QY 61 MKVEREIAILKLEHHPVLKLDVYENKKYLYLVLEHVSQGLFPDYLVKGRILPFXEARK 120
DB 61 MKVEREIAILKLEHHPVLKLDVYENKKYLYLVLEHVSQGLFPDYLVKGRILPFXEARK 120
QY 121 FPROIISALDFCHSHSICHRDLKPEPNLLDEKNRIADFGMASIQVDSLSLETSCGSPH 180
DB 121 FPROIISALDFCHSHSICHRDLKPEPNLLDEKNRIADFGMASIQVDSLSLETSCGSPH 180
QY 181 VACPEVIRGEKYDGKADVSGCVILFALLVGALEPDDDNRLRLLEKXGQVFMHPHPI 240
DB 181 VACPEVIRGEKYDGKADVSGCVILFALLVGALEPDDDNRLRLLEKXGQVFMHPHPI 240
QY 241 PDCOSILRGMEYVDAAARLTLLEHIGKIWIYIGKNEPEPEPIPRKVOIRSLPSLEIDIP 300
DB 241 PDCOSILRGMEYVDAAARLTLLEHIGKIWIYIGKNEPEPEPIPRKVOIRSLPSLEIDIP 300
QY 301 DVLDSMHSIGCFRDNNKLLODLSSEENOEKVIYFLLLDRKERYPSQDEDELPPNNEIDP 360
DB 301 DVLDSMHSIGCFRDNNKLLODLSSEENOEKVIYFLLLDRKERYPSQDEDELPPNNEIDP 360
QY 361 PRKRVDSYMLNRHGKRRPKSKMEVLYSTVDGSPVPARAIEMAHGQRSSISGASGSL 420
DB 361 PRKRVDSYMLNRHGKRRPKSKMEVLYSTVDGSPVPARAIEMAHGQRSSISGASGSL 420
QY 421 STSPLSRPVTPHPSPRGSPPLTPKGTVPHTPKESPACTNPNTPPSSPSVGVGVPWRARLN 480
DB 421 STSPLSRPVTPHPSPRGSPPLTPKGTVPHTPKESPACTNPNTPPSSPSVGVGVPWRARLN 480

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QY 481 SIKNSFLGSPRRHRRKQVPTPEMSNLTPESSPELAKKSGFNGFTSLEKEQIFVVIKD 540
DB 481 SIKNSFLGSPRRHRRKQVPTPEMSNLTPESSPELAKKSGFNGFTSLEKEQIFVVIKD 540
QY 541 KPLSSIKADIYHAFSLISLSHSVTSQTSFRAEYKATGPAVFOQPVKFOVDITYTEGGE 600
DB 541 KPLSSIKADIYHAFSLISLSHSVTSQTSFRAEYKATGPAVFOQPVKFOVDITYTEGGE 600
QY 601 AOKENGIVSVTFTLLSGSPRRFRKRVETIQOQLSTHDPAAQHLSD 647
DB 601 AOKENGIVSVTFTLLSGSPRRFRKRVETIQOQLSTHDPAAQHLSD 647

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## RESULT 7

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US-09-842-582-2
; Sequence 2, Application US/09842582
; Patent No. US20020155570A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 2246. NOVEL PROTEIN KINASE MOLECULES AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 38155-20054.00
; CURRENT APPLICATION NUMBER: US/09/842,582
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/159,391
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-582-2

```

Query Match 96.5%; Score 3374; DB 9; Length 674;

Best Local Similarity 99.7%; Pred. No. 7.9e-210;

Matches 645; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSTGKDGGAQHAQVGYRLEKTLGKQTLGVKLGVCVTCQKVAIKIVREKLSSEVL 60
DB 1 MSTGKDGGAQHAQVGYRLEKTLGKQTLGVKLGVCVTCQKVAIKIVREKLSSEVL 60
QY 61 MKVEREIALIKLIEHPVTLKLDVYENKRYLYVLEHVSQGEIPDYLVKKGRLLTPKEARK 120
DB 61 MKVEREIALIKLIEHPVTLKLDVYENKRYLYVLEHVSQGEIPDYLVKKGRLLTPKEARK 120
QY 121 FFRQITISALDFCHSHSICRDLKPENLIDPEKNIRIADFGMASLQVGSILLETSCGSPH 180
DB 121 FFRQITISALDFCHSHSICRDLKPENLIDPEKNIRIADFGMASLQVGSILLETSCGSPH 180
QY 121 FFRQITISALDFCHSHSICRDLKPENLIDPEKNIRIADFGMASLQVGSILLETSCGSPH 180
DB 121 FFRQITISALDFCHSHSICRDLKPENLIDPEKNIRIADFGMASLQVGSILLETSCGSPH 180
QY 181 YACPEVIRGEKXDDGRKADVMSGVILFALLVGALEPDDDNRLQLLEKXRGVFMHPFIP 240
DB 181 YACPEVIRGEKXDDGRKADVMSGVILFALLVGALEPDDDNRLQLLEKXRGVFMHPFIP 240
QY 241 PDQOSILRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPLEDIDP 300
DB 241 PDQOSILRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPLEDIDP 300
QY 241 PDQOSILRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPLEDIDP 300
DB 241 PDQOSILRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPLEDIDP 300
QY 301 DVLDSMHSIGCFRRNKLQDLSEENQEKIYFLLDRKERYPSQEDDELPRNEIDP 360
DB 301 DVLDSMHSIGCFRRNKLQDLSEENQEKIYFLLDRKERYPSQEDDELPRNEIDP 360
QY 361 PRKRVDSPMLNRHGRRERKSMETLSVTDGGSVPARARAIEMAOHGQRSSISGASGGL 420
DB 361 PRKRVDSPMLNRHGRRERKSMETLSVTDGGSVPARARAIEMAOHGQRSSISGASGGL 420
QY 421 STSPSSSRVTPHSPRGSPLPTPKGTPVHTPKESPACTPVPPTPPSSPVGVPMARLN 480
DB 421 STSPSSSRVTPHSPRGSPLPTPKGTPVHTPKESPACTPVPPTPPSSPVGVPMARLN 480
QY 481 SIKNSFLGSPRRHRRKQVPTPEMSNLTPESSPELAKKSGFNGFTSLEKEQIFVVIKD 540
DB 481 SIKNSFLGSPRRHRRKQVPTPEMSNLTPESSPELAKKSGFNGFTSLEKEQIFVVIKD 540

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DB 481 SIKNSFLGSPRRHRRKQVPTPEMSNLTPESSPELAKKSGFNGFTSLEKEQIFVVIKD 540
QY 541 KPLSSIKADIYHAFSLISLSHSVTSQTSFRAEYKATGPAVFOQPVKFOVDITYTEGGE 600
DB 541 KPLSSIKADIYHAFSLISLSHSVTSQTSFRAEYKATGPAVFOQPVKFOVDITYTEGGE 600
QY 601 AOKENGIVSVTFTLLSGSPRRFRKRVETIQOQLSTHDPAAQHLSD 647
DB 601 AOKENGIVSVTFTLLSGSPRRFRKRVETIQOQLSTHDPAAQHLSD 647

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## RESULT 8

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US-10-283-247-7
; Sequence 7, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-283-247-7

```

Query Match 96.5%; Score 3374; DB 14; Length 674;

Best Local Similarity 99.7%; Pred. No. 7.9e-210;

Matches 645; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MSTGKDGGAQHAQVGYRLEKTLGKQTLGVKLGVCVTCQKVAIKIVREKLSSEVL 60
DB 1 MSTGKDGGAQHAQVGYRLEKTLGKQTLGVKLGVCVTCQKVAIKIVREKLSSEVL 60
QY 61 MKVEREIALIKLIEHPVTLKLDVYENKRYLYVLEHVSQGEIPDYLVKKGRLLTPKEARK 120
DB 61 MKVEREIALIKLIEHPVTLKLDVYENKRYLYVLEHVSQGEIPDYLVKKGRLLTPKEARK 120
QY 121 FFRQITISALDFCHSHSICRDLKPENLIDPEKNIRIADFGMASLQVGSILLETSCGSPH 180
DB 121 FFRQITISALDFCHSHSICRDLKPENLIDPEKNIRIADFGMASLQVGSILLETSCGSPH 180
QY 181 YACPEVIRGEKXDDGRKADVMSGVILFALLVGALEPDDDNRLQLLEKXRGVFMHPFIP 240
DB 181 YACPEVIRGEKXDDGRKADVMSGVILFALLVGALEPDDDNRLQLLEKXRGVFMHPFIP 240
QY 241 PDQOSILRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPLEDIDP 300
DB 241 PDQOSILRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPLEDIDP 300
QY 241 PDQOSILRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPLEDIDP 300
DB 241 PDQOSILRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPLEDIDP 300
QY 301 DVLDSMHSIGCFRRNKLQDLSEENQEKIYFLLDRKERYPSQEDDELPRNEIDP 360
DB 301 DVLDSMHSIGCFRRNKLQDLSEENQEKIYFLLDRKERYPSQEDDELPRNEIDP 360
QY 361 PRKRVDSPMLNRHGRRERKSMETLSVTDGGSVPARARAIEMAOHGQRSSISGASGGL 420
DB 361 PRKRVDSPMLNRHGRRERKSMETLSVTDGGSVPARARAIEMAOHGQRSSISGASGGL 420
QY 421 STSPSSSRVTPHSPRGSPLPTPKGTPVHTPKESPACTPVPPTPPSSPVGVPMARLN 480
DB 421 STSPSSSRVTPHSPRGSPLPTPKGTPVHTPKESPACTPVPPTPPSSPVGVPMARLN 480
QY 481 SIKNSFLGSPRRHRRKQVPTPEMSNLTPESSPELAKKSGFNGFTSLEKEQIFVVIKD 540
DB 481 SIKNSFLGSPRRHRRKQVPTPEMSNLTPESSPELAKKSGFNGFTSLEKEQIFVVIKD 540
QY 541 KPLSSIKADIYHAFSLISLSHSVTSQTSFRAEYKATGPAVFOQPVKFOVDITYTEGGE 600
DB 541 KPLSSIKADIYHAFSLISLSHSVTSQTSFRAEYKATGPAVFOQPVKFOVDITYTEGGE 600

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Db 541 KPSSIKADIYAHAFILPSLSHSVITQTFRAEYKATGPAVFOQVQVDTITTEGE 600  
Qy 601 AQKENGIVSVTFTLLSGPSRRFRKVVETIOAQLLSTHDPAAQHLS 647  
Db 601 AQKENGIVSVTFTLLSGPSRRFRKVVETIOAQLLSTHDPAAQHLS 647

RESULT 9  
US-10-283-247-8  
; Sequence 8, Application US/10283247  
; Publication No. US20030119037A1  
; GENERAL INFORMATION:  
; APPLICANT: NEELEAM, Beera et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001304  
; CURRENT APPLICATION NUMBER: US/10/283,247  
; CURRENT FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-283-247-8

Query Match 96.5%; Score 3374; DB 14; Length 674;  
Best Local Similarity 99.7%; Pred. No. 7,9e-210;  
Matches 645; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MTSIGKDGGAQHAYVAPYRLKLTGKGTGLVAVGVHCVTQKVAIKIVNREKSESVL 60  
Db 1 MTSIGKDGGAQHAYVAPYRLKLTGKGTGLVAVGVHCVTQKVAIKIVNREKSESVL 60  
Qy 61 MKYERETAILKLEHPIVHLKLDHYENKLYLVLEHVSQSGELFDYLVKKGRLTPGEAKX 120  
Db 61 MKYERETAILKLEHPIVHLKLDHYENKLYLVLEHVSQSGELFDYLVKKGRLTPGEAKX 120  
Qy 121 FFRQIISALDFCHSHSICHRDLKPEMLLDKNNIRIADFGMASLQVGDLSLETSCGSPH 180  
Db 121 FFRQIISALDFCHSHSICHRDLKPEMLLDKNNIRIADFGMASLQVGDLSLETSCGSPH 180  
Qy 181 YACEVTRGEXYDGRKADVWSCGYILFALLVGAALPPDDNLRQLLEKVRGVMHMFIP 240  
Db 181 YACEVTRGEXYDGRKADVWSCGYILFALLVGAALPPDDNLRQLLEKVRGVMHMFIP 240  
Qy 241 PDCOSILRGMIENVDAARLTLEHIQKAIWYIGKNEPEPEQPIPRKVOIRSLPSLEIDIP 300  
Db 241 PDCOSILRGMIENVDAARLTLEHIQKAIWYIGKNEPEPEQPIPRKVOIRSLPSLEIDIP 300  
Qy 301 DVLDSMHSIGCFDRNKLLODLLSEENOEKMIYFLLDRKERYPSQEDDLPRNEIDIP 360  
Db 301 DVLDSMHSIGCFDRNKLLODLLSEENOEKMIYFLLDRKERYPSQEDDLPRNEIDIP 360  
Qy 361 PRKVDSPMLNRHGRKRRPERKSMVELSVTGGSPVPRARAIEMAHQGRSRISGASSGI 420  
Db 361 PRKVDSPMLNRHGRKRRPERKSMVELSVTGGSPVPRARAIEMAHQGRSRISGASSGI 420  
Qy 421 STPLSPFRVTPHSPRGSPLPTPKGTVMHTPKESPAGTNPPTPSSPSVGVPMWRAILN 480  
Db 421 STPLSPFRVTPHSPRGSPLPTPKGTVMHTPKESPAGTNPPTPSSPSVGVPMWRAILN 480  
Qy 481 SIKKSFUSGPRFHRKQVPTPEEMSNLTPESSPELAKKSMFGNFIISLEKEBOIFVYIKD 540  
Db 481 SIKKSFUSGPRFHRKQVPTPEEMSNLTPESSPELAKKSMFGNFIISLEKEBOIFVYIKD 540  
Qy 541 KPLSSIKADIYAHAFILPSLSHSVITQTFRAEYKATGPAVFOQVQVDTITTEGE 600  
Db 541 KPLSSIKADIYAHAFILPSLSHSVITQTFRAEYKATGPAVFOQVQVDTITTEGE 600  
Qy 601 AQKENGIVSVTFTLLSGPSRRFRKVVETIOAQLLSTHDPAAQHLS 647

Db 601 AQKENGIVSVTFTLLSGPSRRFRKVVETIOAQLLSTHDPAAQHLS 647

RESULT 10  
US-10-425-114-54467  
; Sequence 54467, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 54467  
; LENGTH: 688  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB4651-024-E4\_FLI.pep  
US-10-425-114-54467

Query Match 91.5%; Score 3200; DB 12; Length 688;  
Best Local Similarity 96.1%; Pred. No. 1,4e-198;  
Matches 616; Conservative 2; Mismatches 1; Indels 22; Gaps 1;  
Qy 29 QTVGVKGVHCVTQKVAIKIVNREKSESVIMKVEREIAILKLEHPIVHLKLDHYENK 88  
Db 21 RAGLVKGVHCVTQKVAIKIVNREKSESVIMKVEREIAILKLEHPIVHLKLDHYENK 80  
Qy 89 KYLVLEHVSQSGELFDYLVKKGRLTPGEAKRFRQIISALDFCHSHSICHRDLKPEMLL 148  
Db 81 KYLVLEHVSQSGELFDYLVKKGRLTPGEAKRFRQIISALDFCHSHSICHRDLKPEMLL 140  
Qy 149 LDEKNNIRIADFGMASLQVGDLSLETSCGSPHVAQCEVINGEKYDGRKADVWSCGYILFA 208  
Db 141 LDEKNNIRIADFGMASLQVGDLSLETSCGSPHVAQCEVINGEKYDGRKADVWSCGYILFA 200  
Qy 209 LTVGALPPDDNLRQLLEKVRGVMHMFIPDCOSILRGMIENVDAARLTLEHIQKI 268  
Db 201 LTVGALPPDDNLRQLLEKVRGVMHMFIPDCOSILRGMIENVDAARLTLEHIQKI 260  
Qy 269 WYIGKNEPEPEQPIPRKVOIRSLPSLEIDIPDVLDSHSGCFDRNKLLODLLSEEN 328  
Db 261 WYIGKNEPEPEQPIPRKVOIRSLPSLEIDIPDVLDSHSGCFDRNKLLODLLSEEN 320  
Qy 329 QEKMIYFLLDRKERYPSQEDDLPRNEIDIPPRKVDSPMLNRHGRKRRPERKSMVELSV 388  
Db 321 QEKMIYFLLDRKERYPSQEDDLPRNEIDIPPRKVDSPMLNRHGRKRRPERKSMVELSV 380  
Qy 389 TDGSPVPRARAIEMAHQGRSRISGASSGI 426  
Db 381 TDGSPVPRARAIEMAHQGRSRISGASSGI 440  
Qy 427 SPRVTPHSPRGSPLPTPKGTVMHTPKESPAGTNPPTPSSPSVGVPMWRAILN 486  
Db 441 SPRVTPHSPRGSPLPTPKGTVMHTPKESPAGTNPPTPSSPSVGVPMWRAILN 500  
Qy 487 LGSPPFRHKKQVPTPEEMSNLTPESSPELAKKSMFGNFIISLEKEBOIFVYIKD 546  
Db 501 LGSPPFRHKKQVPTPEEMSNLTPESSPELAKKSMFGNFIISLEKEBOIFVYIKD 560  
Qy 547 KADIYAHAFILPSLSHSVITQTFRAEYKATGPAVFOQVQVDTITTEGE 606  
Db 561 KADIYAHAFILPSLSHSVITQTFRAEYKATGPAVFOQVQVDTITTEGE 620

QY 607 IYVTFLLSGPSRRFRKRVETIOQLLSTHDPAAQHLSD 647  
 DB 621 IYVTFLLSGPSRRFRKRVETIOQLLSTHDPAAQHLSE 661

## RESULT 11

US-10-054-579-4  
 ; Sequence 4, Application US/10054579  
 ; Publication No. US20020137913A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Mathur, Brian  
 ; TITLE OF INVENTION: No. US20020137913A1 Human Kinases and Polynucleotides Encoding  
 ; FILE REFERENCE: LEX-0300-USA  
 ; CURRENT APPLICATION NUMBER: US/10/054,579  
 ; CURRENT FILING DATE: 2002-01-22  
 ; PRIOR APPLICATION NUMBER: US 60/263,378  
 ; PRIOR FILING DATE: 2001-01-23  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 608  
 ; TYPE: PR1  
 ; ORGANISM: homo sapiens  
 US-10-054-579-4

Query Match 91.2%; Score 3188; DB 13; Length 608;  
 Best Local Similarity 100.0%; Pred. No. 7,4e-198;  
 Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 MKVEREIALIKLIEHPVTKLHDVYENKCYLYLVLEHVSQGEIPDYLVKKGRITPEARK 120  
 DB 1 MKVEREIALIKLIEHPVTKLHDVYENKCYLYLVLEHVSQGEIPDYLVKKGRITPEARK 60  
 QY 121 FFRQIISALDFCHSHSICRDLKPEKNTLLDEKNNIRIADFGMASIQVDSILLETSCGSPH 180  
 DB 61 FFRQIISALDFCHSHSICRDLKPEKNTLLDEKNNIRIADFGMASIQVDSILLETSCGSPH 120  
 QY 181 YACPEVIRGEXYDGRKADVSCGYLLFALLVGALEPDDNLRQLLEKVRGVFHMHPFIP 240  
 DB 121 YACPEVIRGEXYDGRKADVSCGYLLFALLVGALEPDDNLRQLLEKVRGVFHMHPFIP 180  
 QY 241 PDCQSLRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPSEIDIP 300  
 DB 181 PDCQSLRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPSEIDIP 240  
 QY 301 DVLDSMHSIGCFRDRNKLQDLSEBENOEKMIYFLLDRKERYPSQEDDELPRNEIDIP 360  
 DB 241 DVLDSMHSIGCFRDRNKLQDLSEBENOEKMIYFLLDRKERYPSQEDDELPRNEIDIP 300  
 QY 361 PRKRVDSFMLNRGKRPERKSMEVLSVTDGSPVPARRAIEMAOHGORSISGASGL 420  
 DB 301 PRKRVDSFMLNRGKRPERKSMEVLSVTDGSPVPARRAIEMAOHGORSISGASGL 360  
 QY 421 STPLSSPRVTPHSPRSGPLPTPKGTPVHTPKESPAGTPNPPTPSSPSVGVPMRARN 480  
 DB 361 STPLSSPRVTPHSPRSGPLPTPKGTPVHTPKESPAGTPNPPTPSSPSVGVPMRARN 420  
 QY 481 STKNSFLGSPFRFRKQVPTPEEMSNLTPESSPELAKKSWFGNFTLSKEKEQIFVYIKD 540  
 DB 421 STKNSFLGSPFRFRKQVPTPEEMSNLTPESSPELAKKSWFGNFTLSKEKEQIFVYIKD 480  
 QY 541 KPLSSIKADIYHAFSLPSLSHVSISQTSFRAEYKATGGPAVFOKPVKQVQDITYTTEGGE 600  
 DB 481 KPLSSIKADIYHAFSLPSLSHVSISQTSFRAEYKATGGPAVFOKPVKQVQDITYTTEGGE 540  
 QY 601 AOKENGISYVTFLLSGPSRRFRKRVETIOQLLSTHDPAAQHLSDITNCHEMTGRLS 660  
 DB 541 AOKENGISYVTFLLSGPSRRFRKRVETIOQLLSTHDPAAQHLSDITNCHEMTGRLS 600  
 QY 661 KCGIIPKS 668  
 DB 601 KCGIIPKS 608

## RESULT 12

US-10-283-247-9  
 ; Sequence 9, Application US/10283247  
 ; Publication No. US20030119037A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NEELAM, Beena et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; FILE REFERENCE: CLO01304  
 ; CURRENT APPLICATION NUMBER: US/10/283,247  
 ; CURRENT FILING DATE: 2002-10-30  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 614  
 ; TYPE: PR1  
 ; ORGANISM: Homo sapiens  
 US-10-283-247-9

Query Match 87.6%; Score 3065; DB 14; Length 614;  
 Best Local Similarity 99.7%; Pred. No. 6.8e-190;  
 Matches 585; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 61 MKVEREIALIKLIEHPVTKLHDVYENKCYLYLVLEHVSQGEIPDYLVKKGRITPEARK 120  
 DB 1 MKVEREIALIKLIEHPVTKLHDVYENKCYLYLVLEHVSQGEIPDYLVKKGRITPEARK 60  
 QY 121 FFRQIISALDFCHSHSICRDLKPEKNTLLDEKNNIRIADFGMASIQVDSILLETSCGSPH 180  
 DB 61 FFRQIISALDFCHSHSICRDLKPEKNTLLDEKNNIRIADFGMASIQVDSILLETSCGSPH 120  
 QY 181 YACPEVIRGEXYDGRKADVSCGYLLFALLVGALEPDDNLRQLLEKVRGVFHMHPFIP 240  
 DB 121 YACPEVIRGEXYDGRKADVSCGYLLFALLVGALEPDDNLRQLLEKVRGVFHMHPFIP 180  
 QY 241 PDCQSLRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPSEIDIP 300  
 DB 181 PDCQSLRGMIEVDAAARLTLEHIQKHIWYIGKNEPEPEOPIPRKVQIRSLPSEIDIP 240  
 QY 301 DVLDSMHSIGCFRDRNKLQDLSEBENOEKMIYFLLDRKERYPSQEDDELPRNEIDIP 360  
 DB 241 DVLDSMHSIGCFRDRNKLQDLSEBENOEKMIYFLLDRKERYPSQEDDELPRNEIDIP 300  
 QY 361 PRKRVDSFMLNRGKRPERKSMEVLSVTDGSPVPARRAIEMAOHGORSISGASGL 420  
 DB 301 PRKRVDSFMLNRGKRPERKSMEVLSVTDGSPVPARRAIEMAOHGORSISGASGL 360  
 QY 421 STPLSSPRVTPHSPRSGPLPTPKGTPVHTPKESPAGTPNPPTPSSPSVGVPMRARN 480  
 DB 361 STPLSSPRVTPHSPRSGPLPTPKGTPVHTPKESPAGTPNPPTPSSPSVGVPMRARN 420  
 QY 481 STKNSFLGSPFRFRKQVPTPEEMSNLTPESSPELAKKSWFGNFTLSKEKEQIFVYIKD 540  
 DB 421 STKNSFLGSPFRFRKQVPTPEEMSNLTPESSPELAKKSWFGNFTLSKEKEQIFVYIKD 480  
 QY 541 KPLSSIKADIYHAFSLPSLSHVSISQTSFRAEYKATGGPAVFOKPVKQVQDITYTTEGGE 600  
 DB 481 KPLSSIKADIYHAFSLPSLSHVSISQTSFRAEYKATGGPAVFOKPVKQVQDITYTTEGGE 540  
 QY 601 AOKENGISYVTFLLSGPSRRFRKRVETIOQLLSTHDPAAQHLSD 647  
 DB 541 AOKENGISYVTFLLSGPSRRFRKRVETIOQLLSTHDPAAQHLSE 587

## RESULT 13

US-10-283-247-10  
 ; Sequence 10, Application US/10283247  
 ; Publication No. US20030119037A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NEELAM, Beena et al.



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; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROOF
; FILE REFERENCE: CLO01304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-283-247-10

```

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Query Match      87.6%; Score 3065; DB 14; Length 614;
Best Local Similarity 99.7%; Pred. No. 6,86-130;
Matches 565; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 61 MKVEREIAIKLIEHPVILKLDHYENKXYLYLLEHVSGGELFDYLYKKGRITPEAKR 120
DB 1 MKVEREIAIKLIEHPVILKLDHYENKXYLYLLEHVSGGELFDYLYKKGRITPEAKR 60
QY 121 FFRQIISALDFCHSHSICRDLKPENLLDEKNIRIADFGMASLOVGSILSTSCGSPH 180
DB 61 FFRQIISALDFCHSHSICRDLKPENLLDEKNIRIADFGMASLOVGSILSTSCGSPH 120
QY 181 YACPEVIRGEKYGKADVWSCGVILPALLVGALEPDDNLRQLLEKRGVFNHMFIP 240
DB 121 YACPEVIRGEKYGKADVWSCGVILPALLVGALEPDDNLRQLLEKRGVFNHMFIP 180
QY 241 PDCQSLRGMI EVDAAARLTLEHIQKHVIYIGKNEPEPEOPIPRKVQIRSLPSLEIDIP 300
DB 181 PDCQSLRGMI EVDAAARLTLEHIQKHVIYIGKNEPEPEOPIPRKVQIRSLPSLEIDIP 240
QY 301 DVLDSMHSIGCFRDRNKLQDLISEEENOEKMIYFLLDRKERYPQOEDEDLPPENEIDP 360
DB 241 DVLDSMHSIGCFRDRNKLQDLISEEENOEKMIYFLLDRKERYPQOEDEDLPPENEIDP 300
QY 361 PRKRVDSPLNLRHGKRPERSKMEVLSVTDGSPVPARAIEMAHQGRSISGASGL 420
DB 301 PRKRVDSPLNLRHGKRPERSKMEVLSVTDGSPVPARAIEMAHQGRSISGASGL 360
QY 421 STSPSSPRVTPHPSRPGSPLPPTKGTVPHTPKESPAGTNPPTPSSPSVGVPMARIN 480
DB 361 STSPSSPRVTPHPSRPGSPLPPTKGTVPHTPKESPAGTNPPTPSSPSVGVPMARIN 420
QY 481 SIKNSFLGSPRFRHKKLOVPTPEEMSNLTPESSPELAKSGMFGNFISLEKEQIFVYID 540
DB 421 SIKNSFLGSPRFRHKKLOVPTPEEMSNLTPESSPELAKSGMFGNFISLEKEQIFVYID 480
QY 541 KPUSIKADIYHAFILSPISLSHVSISQTSFPAEYKATGPAVFOKPVKQVDITYEGGE 600
DB 481 KPUSIKADIYHAFILSPISLSHVSISQTSFPAEYKATGPAVFOKPVKQVDITYEGGE 540
QY 601 AOKENGIVSVFTLLSGSPRFRKRVETIOAQLLSTHDPAAQHLS 647
DB 541 AOKENGIVSVFTLLSGSPRFRKRVETIOAQLLSTHDPAAQHLS 587

```

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RESULT 14
US-10-283-247-5
; Sequence 5, Application US/10283247
; Publication No. US20030119037A1
; GENERAL INFORMATION:
; APPLICANT: NEBELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01304
; CURRENT APPLICATION NUMBER: US/10/283,247
; CURRENT FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 5
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-283-247-5

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Query Match      87.2%; Score 3050; DB 14; Length 636;
Best Local Similarity 96.2%; Pred. No. 6,66-189;
Matches 586; Conservative 1; Mismatches 0; Indels 22; Gaps 1;

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QY 61 MKVEREIAIKLIEHPVILKLDHYENKXYLYLLEHVSGGELFDYLYKKGRITPEAKR 120
DB 1 MKVEREIAIKLIEHPVILKLDHYENKXYLYLLEHVSGGELFDYLYKKGRITPEAKR 60
QY 121 FFRQIISALDFCHSHSICRDLKPENLLDEKNIRIADFGMASLOVGSILSTSCGSPH 180
DB 61 FFRQIISALDFCHSHSICRDLKPENLLDEKNIRIADFGMASLOVGSILSTSCGSPH 120
QY 181 YACPEVIRGEKYGKADVWSCGVILPALLVGALEPDDNLRQLLEKRGVFNHMFIP 240
DB 121 YACPEVIRGEKYGKADVWSCGVILPALLVGALEPDDNLRQLLEKRGVFNHMFIP 180
QY 241 PDCQSLRGMI EVDAAARLTLEHIQKHVIYIGKNEPEPEOPIPRKVQIRSLPSLEIDIP 300
DB 181 PDCQSLRGMI EVDAAARLTLEHIQKHVIYIGKNEPEPEOPIPRKVQIRSLPSLEIDIP 240
QY 301 DVLDSMHSIGCFRDRNKLQDLISEEENOEKMIYFLLDRKERYPQOEDEDLPPENEIDP 360
DB 241 DVLDSMHSIGCFRDRNKLQDLISEEENOEKMIYFLLDRKERYPQOEDEDLPPENEIDP 300
QY 361 PRKRVDSPLNLRHGKRPERSKMEVLSVTDGSPVPARAIEMAHQGRSISGASGL 420
DB 301 PRKRVDSPLNLRHGKRPERSKMEVLSVTDGSPVPARAIEMAHQGRSISGASGL 360
QY 409 -----RSRSISGASGLSTSPSSPRVTPHPSRPGSPLPPTKGTVPHTPKESPAG 458
DB 361 EAHQFQSKEDRSRSISGASGLSTSPSSPRVTPHPSRPGSPLPPTKGTVPHTPKESPAG 420
QY 459 TPNTTPSSPSVGVPMARINIKNSFLGSPRFRHKKLOVPTPEEMSNLTPESSPELAK 518
DB 421 TPNTTPSSPSVGVPMARINIKNSFLGSPRFRHKKLOVPTPEEMSNLTPESSPELAK 480
QY 519 KSMFGNLSLEKEQIFVYIKDPLSSIKADIYHAFILSPISLSHVSISQTSFPAEYKATG 578
DB 481 KSMFGNLSLEKEQIFVYIKDPLSSIKADIYHAFILSPISLSHVSISQTSFPAEYKATG 540
QY 579 GPAVFOKPVKQVDITYEGGEAOKENGIVSVFTLLSGSPRFRKRVETIOAQLLSTHD 638
DB 541 GPAVFOKPVKQVDITYEGGEAOKENGIVSVFTLLSGSPRFRKRVETIOAQLLSTHD 600
QY 639 PPAQHLS 647
DB 601 PPAQHLS 609

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RESULT 15
US-10-195-072-4
; Sequence 4, Application US/10195072
; Publication No. US20030092036A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Full-length Serine Protein Kinase in Brain and Pancreas
; FILE REFERENCE: 16U 101 C2
; CURRENT APPLICATION NUMBER: US/10/195,072
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 09/930,181
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-195-072-4

Query Match	86.6%;	Score 3028;	DB 14;	Length 585;
Best Local Similarity	100.0%;	Pred. No. 1.6e-187;		
Matches 577;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	92	YLVEHVS	GGEGLF	YL	VKKR	LTLP	PK	KAR	FFR	II	SLAD	FG	SHS	I	GRD	X	KN	PE	LL	DE	151
Db	9	YLVEHVS	GGEGL	ED	YL	VKKR	LTLP	KAR	FFR	II	SLAD	FG	SHS	I	GRD	X	KN	PE	LL	DE	68
QY	152	KN	RI	AD	FG	MA	S	IQ	VG	DS	LL	ETS	SC	SP	YAC	EV	I	R	G	X	211
Db	69	KN	RI	AD	FG	MA	S	IQ	VG	DS	LL	ETS	SC	SP	YAC	EV	I	R	G	X	128
QY	212	GAL	F	DD	DN	I	R	OL	LE	K	Y	K	V	F	FM	P	H	F	I	P	271
Db	129	GAL	F	DD	DN	I	R	OL	LE	K	Y	K	V	F	FM	P	H	F	I	P	188
QY	272	G	K	N	E	P	E	P	E	O	I	R	K	V	I	R	S	L	E	I	331
Db	189	G	K	N	E	P	E	P	E	O	I	R	K	V	I	R	S	L	E	I	248
QY	332	M	I	Y	L	L	D	R	K	E	R	Y	P	S	O	E	D	E	D	L	391
Db	249	M	I	Y	L	L	D	R	K	E	R	Y	P	S	O	E	D	E	D	L	308
QY	392	G	S	P	V	A	R	A	I	E	M	O	H	G	R	S	I	S	I	G	451
Db	309	G	S	P	V	A	R	A	I	E	M	O	H	G	R	S	I	S	I	G	368
QY	452	P	K	S	E	P	A	C	T	P	P	T	S	S	V	G	V	P	A	R	511
Db	369	P	K	S	E	P	A	C	T	P	P	T	S	S	V	G	V	P	A	R	428
QY	512	S	S	P	E	L	A	K	S	W	F	G	N	F	I	S	L	E	K	E	571
Db	429	S	S	P	E	L	A	K	S	W	F	G	N	F	I	S	L	E	K	E	488
QY	572	A	E	V	A	T	G	G	P	A	V	F	O	K	P	Y	F	O	D	I	631
Db	489	A	E	V	A	T	G	G	P	A	V	F	O	K	P	Y	F	O	D	I	548
QY	632	Q	L	I	S	T	H	D	P	P	A	O	H	L	S	T	I	N	C	M	668
Db	549	Q	L	I	S	T	H	D	P	P	A	O	H	L	S	T	I	N	C	M	585

Search completed: July 29, 2004, 10:32:11  
Job time : 51 secs

